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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 19:18:54 ; Search time 3648 Seconds
(without alignments)

12292.993 Million cell updates/sec

Title: US-10-798-896-1

Perfect score: 5423

Sequence: 1 ccaccgggtggcgccgctc.....ctatagggaattggagct 5423

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.Main.*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
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- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5423	100.0	5423	9	US-10-798-896-1
2	2237	41.3	2237	9	US-10-798-896-5
3	2218	40.9	3599	3	US-09-861-101-3
4	2218	40.9	3803	9	US-10-798-896-2
5	2215.8	40.9	3600	3	US-09-861-101-2
6	2211.6	40.8	3558	7	US-10-281-067B-26
7	2211.6	40.8	3558	8	US-10-764-818A-26
8	2160	39.8	2192	5	US-10-021-403A-10
9	2160	39.8	3534	5	US-10-021-403A-9
10	2160	39.8	3534	7	US-10-395-709-11
11	2160	39.8	3534	7	US-10-395-709-12
12	2160	39.8	3534	7	US-10-395-709-13
13	2160	39.8	3534	7	US-10-395-709-14
14	2160	39.8	3534	7	US-10-395-709-15
15	2160	39.8	3534	7	US-10-359-919A-11
16	2160	39.8	3534	7	US-10-359-919A-12
17	2160	39.8	3534	7	US-10-359-919A-13
18	2160	39.8	3534	7	US-10-359-919A-14
19	2160	39.8	3534	7	US-10-359-919A-15
20	2160	39.8	3534	7	US-10-315-907A-11
21	2160	39.8	3534	7	US-10-315-907A-12
22	2160	39.8	3534	7	US-10-315-907A-13
23	2160	39.8	3534	7	US-10-315-907A-14

ALIGNMENTS

RESULT 1

US-10-798-896-1

; Sequence 1, Application US/10798896

; Publication No. US20050238624A1

; GENERAL INFORMATION:

; APPLICANT: ADVISYS, Inc.

; TITLE OF INVENTION: Insulin-Like Growth Factor ("IGF-I") Plasmid Mediated Supplementa

; TITLE OF INVENTION: Therapeutic Applications

; FILE REFERENCE: 108328.00172 - AVSI-0034

; CURRENT APPLICATION NUMBER: US/10798,896

; CURRENT FILING DATE: 2004-03-11

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 5423

; TYPE: DNA

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: Nucleic acid sequence for the pAV2001 plasmid.

US-10-798-896-1

Query Match	100.0%;	Score 5423;	DB 9;	Length 5423;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 5423;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CCACCGCGGTGGCGCGGTCCGCCCTCGGCACCATCTCAGCACCCCAATATGGCGAC	60	
Db	1	CCACCGCGGTGGCGCGGTCCGCCCTCGGCACCATCTCAGCACCCCAATATGGCGAC	60	
Qy	61	GGGTGAGGAATGTGGGGAGTTATTTTAGAGCGGTGAGGAAGTGGCGAGGACGAGGT	120	
Db	61	GGGTGAGGAATGTGGGGAGTTATTTTAGAGCGGTGAGGAAGTGGCGAGGACGAGGT	120	
Qy	121	GTGGCGGTCTAAAAATAAATCTCCGGAGTTATTTTAGAGCGGAGGAATGGTGACACC	180	
Db	121	GTGGCGGTCTAAAAATAAATCTCCGGAGTTATTTTAGAGCGGAGGAATGGTGACACC	180	
Qy	181	CAATATGGCGAGGTTCCTCACCGTGCATATTTGGGTGTCGCCCTCGCGCGGGGC	240	
Db	181	CAATATGGCGAGCGTTCCTCACCGTGCATATTTGGGTGTCGCCCTCGCGCGGGGC	240	
Qy	241	CGCATTTCTGGGGCGCGCGGTGCTCCCGCCCGCTCCGATAAAGGCTCCGGGGCGGC	300	
Db	241	CGCATTTCTGGGGCGCGCGGTGCTCCCGCCCGCTCCGATAAAGGCTCCGGGGCGGC	300	
Qy	301	GGCGGCCACAGACTACCCGGAGGAGCGGAGCGCAAGCTCTAGAACTAGTGGATCCC	360	

Db	1021	GGGACGACCTGCTGGGAAGAAAAGATGATTTTCAACTGAACTTACTATCAGCGCGTTA	1080
Qy	2014	TTGCTTTATTTGTGATGCTGTAAAGAGTGCCTTTCTCTCACTGTAAATGATTTTGGCCCTCA	2073
Db	1081	TTGCTTTATTTGTGATGCTGTAAAGAGTGCCTTTCTCTCACTGTAAATGATTTTGGCCCTCA	1140
Qy	2074	TGTGTGAAATACACTTTTCCAAATAACAGACACAGCCTCCAAAGGGAAATTTCTCGAGGAAGAGA	2133
Db	1141	TGTGTGAAATACACTTTTCCAAATAACAGACACAGCCTCCAAAGGGAAATTTCTCGAGGAAGAGA	1200
Qy	2134	CAGTACCTGTGTGGGAAGTCCCTGTGTCAGCCCTATGTGCTTCAAGCTGAATGGCTGGGA	2193
Db	1201	CAGTACCTGTGTGGGAAGTCCCTGTGTCAGCCCTATGTGCTTCAAGCTGAATGGCTGGGA	1260
Qy	2194	CTGGCTGGGAGAGCAGGATCACATCCTTTCTTAAAAAGACAAACAGAAAGTGTGTGTGA	2253
Db	1261	CTGGCTGGGAGAGCAGGATCACATCCTTTCTTAAAAAGACAAACAGAAAGTGTGTGTGA	1320
Qy	2254	CTTTGCTGTATTTACTATTTACGGTTTGTGTTTCAGTGGCACATACCTCAACGGGGATAT	2313
Db	1321	CTTTGCTGTATTTACTATTTACGGTTTGTGTTTCAGTGGCACATACCTCAACGGGGATAT	1380
Qy	2314	GGAGAGCTATTTCCCAACCCCTGCCTGCTGGACCTGTATCTGGGGTTTTCCTGTAGCTTA	2373
Db	1381	GGAGAGCTATTTCCCAACCCCTGCCTGCTGGACCTGTATCTGGGGTTTTCCTGTAGCTTA	1440
Qy	2374	AGCGGTGCCAACTGCTTAAAGTGAATGAGTAAGTCAAGTAAAGCTCGAAAGACACACAGATCA	2433
Db	1441	AGCGGTGCCAACTGCTTAAAGTGAATGAGTAAGTCAAGTAAAGCTCGAAAGACACACAGATCA	1500
Qy	2434	TTAAGTCCAACTGTGAGCCCCCATCCCAACCGCGCCCACTGTCACTCAGTGCACATCCAC	2493
Db	1501	TTAAGTCCAACTGTGAGCCCCCATCCCAACCGCGCCCACTGTCACTCAGTGCACATCCAC	1560
Qy	2494	GCATTTCTTGAAACATCTCAGAGGACAGTGAATCCACCCGTCACCGCTGCTTCAGAGC	2553
Db	1561	GCATTTCTTGAAACATCTCAGAGGACAGTGAATCCACCCGTCACCGCTGCTTCAGAGC	1620
Qy	2554	AGCAGGGTCACAGTCTCAGTGGCCAGTTGCATCTCTGCTGAAGAGCTTAAACAGTGCAGTTT	2613
Db	1621	AGCAGGGTCACAGTCTCAGTGGCCAGTTGCATCTCTGCTGAAGAGCTTAAACAGTGCAGTTT	1680
Qy	2614	AACAAACGGAAGTGTGATGTTGATGTTGCTGAATCAGTACGTTGAGATGTCACTAAACT	2673
Db	1681	AACAAACGGAAGTGTGATGTTGATGTTGCTGAATCAGTACGTTGAGATGTCACTAAACT	1740
Qy	2674	TTTTGGAGATTAATTTCCAGATGGAAACACATCTCTTAAACCTGAAAACAGGCTTTGATTTG	2733
Db	1741	TTTTGGAGATTAATTTCCAGATGGAAACACATCTCTTAAACCTGAAAACAGGCTTTGATTTG	1800
Qy	2734	GGCTTGGCATTTGCAGAAATTTGAGGAAAAGATTTGTTTGGGAAACAGATGAATGGAAATTC	2793
Db	1801	GGCTTGGCATTTGCAGAAATTTGAGGAAAAGATTTGTTTGGGAAACAGATGAATGGAAATTC	1860
Qy	2794	CACCAAAACAGAAAATTAACACTTACACCAAGTTTGAAGTCTGGTCTTCTGTTCCGATATTTCTT	2853
Db	1861	CACCAAAACAGAAAATTAACACTTACACCAAGTTTGAAGTCTGGTCTTCTGTTCCGATATTTCTT	1920
Qy	2854	AAGAACTCATATCTCTCTCTCTTTGGACAGTGTCTGTGACAGGAGTGGAGGATCA	2913
Db	1921	AAGAACTCATATCTCTCTCTCTTTGGACAGTGTCTGTGACAGGAGTGGAGGATCA	1980
Qy	2914	TCAGGGTCAGATCCTCAGCATCTAGGGATGTGCACTATGTGTGATGGTGACACTTTAGA	2973
Db	1981	TCAGGGTCAGATCCTCAGCATCTAGGGATGTGCACTATGTGTGATGGTGACACTTTAGA	2040
Qy	2974	GAATCTGTTTGAATTTCCCAAGGGCTTTCCCTCTCTTCCATGACAGGGCTCACTATCAGCCCT	3033
Db	2041	GAATCTGTTTGAATTTCCCAAGGGCTTTCCCTCTCTTCCATGACAGGGCTCACTATCAGCCCT	2100
Qy	3034	GAAGTCCAACTTTCTGAACTTCCAGCACCGTCTGTCTCTGTTGGTATGGCTGTTCATAGAGG	3093

Db	2101	GAAGTCCAACTTTCTGAACCTCCAGACCGTCTGCTCTCTGCTGAGGCTGTTCATAGAGG	2160
Qy	3094	CCACAGGAGCTGTAGCCAGGCATGACCTTTTCCAGCCGCTGCTCTGAATCCAGCACTGGT	3153
Db	2161	CCACAGGAGCTGTAGCCAGGCATGACCTTTTCCAGCCGCTGCTCTGAATCCAGCACTGGT	2220
Qy	3154	GGCTGGGAGCAGCTCT	3170
Db	2221	GGCTGGGAGCAGCTCT	2237

RESULT 3

US-09-861-101-3

; Sequence 3, Application US/09861101

; Publication No. US20030018984A1

GENERAL INFORMATION:

APPLICANT: COLEMAN, MICHAEL

DEMAIO, FRANCESCO J.

SCHWARTZ, ROBERT

TITLE OF INVENTION: IGF-1 EXPRESSION SYSTEM AND METHODS OF USE

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/861,101

FILING DATE: 18-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/974,572

FILING DATE: November 19, 1997

APPLICATION NUMBER: 60/031,539

FILING DATE: December 2, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Wardburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 230/185-PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 499-1500

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 3599 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-861-101-3

... ..

QY 3310 ATACGAGCGGAGCATAAAGTGTAAAGCCTTG3GTGCCCTAAATGAGTGAGCTAACTCACA 3369
Db 123 ATACGAGCGGAGCATAAAGTGTAAAGCCTTG3GTGCCCTAAATGAGTGAGCTAACTCACA 182
QY 3370 TTAATTTGCGTTGCGCTCACTGCCCGCTTTTCCAGTTCGGGAAACCTGTCGTGCCAGCTGCAT 3429
Db 183 TTAATTTGCGTTGCGCTCACTGCCCGCTTTTCCAGTTCGGGAAACCTGTCGTGCCAGCTGCAT 242
QY 3430 TAATGAATCGGCCAAACGCGCGGGGAGAGGCGGTTTGGTATTTGGGCGCTCTTCCGCTTCC 3489
Db 243 TAATGAATCGGCCAAACGCGCGGGGAGAGGCGGTTTGGTATTTGGGCGCTCTTCCGCTTCC 302
QY 3490 TCGCTCACTGACTCGCTGCGCTCGCTGCTGCTGCGTGGGAGCGGTATCAGCTCACTCA 3549
Db 303 TCGCTCACTGACTCGCTGCGCTCGCTGCTGCTGCGTGGGAGCGGTATCAGCTCACTCA 362
QY 3550 AAGCGGTAAATACGGTTTATCCACAGAATCAGGGGATAACCGCAGGAAAGAACATGTGAGCA 3609
Db 363 AAGCGGTAAATACGGTTTATCCACAGAATCAGGGGATAACCGCAGGAAAGAACATGTGAGCA 422
QY 3610 AAAGGCCAGCAAAAGGCCAGGAACCGGTAAAGAGGCCGCTGCTGCGGTTTTTCCATAGG 3669
Db 423 AAAGGCCAGCAAAAGGCCAGGAACCGGTAAAGAGGCCGCTGCTGCGGTTTTTCCATAGG 482
QY 3670 CTGCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGTGCGGCAAAACCCG 3729
Db 483 CTGCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGTGCGGCAAAACCCG 542
QY 3730 ACAGGACTATAAAGATACCAAGCGGTTTTCCCGCTTGGAAAGCTCCCTGTCGCGCTCTCTCTGTT 3789
Db 543 ACAGGACTATAAAGATACCAAGCGGTTTTCCCGCTTGGAAAGCTCCCTGTCGCGCTCTCTCTGTT 602
QY 3790 CCSACCTTCGCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGCGGCTT 3849
Db 603 CCSACCTTCGCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGCGGCTT 662
QY 3850 TCTCATAGCTCAGCGTGTAGGTATCTCAGTTCGCTGAGCTCGTTCCGCTCAAGAGCTGGGC 3909
Db 663 TCTCATAGCTCAGCGTGTAGGTATCTCAGTTCGCTGAGCTCGTTCCGCTCAAGAGCTGGGC 722
QY 3910 TGTGTGACGAACCCCGCTTACGCCGACCGCTGCGCTTTATCCGGTAACTATCGTCTT 3969
Db 723 TGTGTGACGAACCCCGCTTACGCCGACCGCTGCGCTTTATCCGGTAACTATCGTCTT 782
QY 3970 GAGTCCAAACCCCGTAAAGACACGACTTATCGCCACTGGCAGCAGCACTGGTAAACAGGATT 4029
Db 783 GAGTCCAAACCCCGTAAAGACACGACTTATCGCCACTGGCAGCAGCACTGGTAAACAGGATT 842
QY 4030 AGCAGAGCGAGGTATGTAGCGGTGTACAGAGTTCTTTGAAGTGGTGGCCCTTAACCTACGGC 4089
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Db 963 AGAGTTGGTGTAGCTTGTATCCGGCAAAACAAACCAACCGCTGGTGGTGGTTTTTTGTT 1022
QY 4210 TGCNAGCAGCAGATTACGCCGAGAAAAGAGATCTCAAGNATCCCTTTGATCTTTCT 4269
Db 1023 TGCNAGCAGCAGATTACGCCGAGAAAAGAGATCTCAAGNATCCCTTTGATCTTTCT 1082
QY 4270 ACGGGGTCTGACGCTCAGAAAGAACTCGCTCAAGAGGCGATAGAGGCGATGCGCTGCGAA 4329
Db 1083 ACGGGGTCTGACGCTCAGAAAGAACTCGCTCAAGAGGCGATAGAGGCGATGCGCTGCGAA 1142
QY 4330 TCGGAGCGCGGATACCGTTAAAGCAGAGGAAGCGGTACGCCCATTCGCCGCCAAGCTCT 4389
Db 1143 TCGGAGCGCGGATACCGTTAAAGCAGAGGAAGCGGTACGCCCATTCGCCGCCAAGCTCT 1202

QY 4390 TCAGCAATATCAGCGGTAGCCAAACGCTATGTCTCTGATAGCGGTCCGCCACACCCAGCCGG 4449
Db 1203 TCAGCAATATCAGCGGTAGCCAAACGCTATGTCTCTGATAGCGGTCCGCCACACCCAGCCGG 1262
QY 4450 CCAACAGTGCATGAATCCAGAAAGCGGCCATTTTTCCACATGATATTCGCAAGACGAGCA 4509
Db 1263 CCAACAGTGCATGAATCCAGAAAGCGGCCATTTTTCCACATGATATTCGCAAGACGAGCA 1322
QY 4510 TCGCCATGGTCAACGAGAGATCTCGCGTGGGCAATCGCGCTTTGAGCCTTGGCGAAC 4569
Db 1323 TCGCCATGGTCAACGAGAGATCTCGCGTGGGCAATCGCGCTTTGAGCCTTGGCGAAC 1382
QY 4570 AGTTCCGCTGGCGAGCGCCCTGATGCTCTTTCGTCAGATCATCTGATCGAACAAGACCG 4629
Db 1383 AGTTCCGCTGGCGAGCGCCCTGATGCTCTTTCGTCAGATCATCTGATCGAACAAGACCG 1442
QY 4630 GCTTCCATCCGAGTACGCTGCTCGATGCGATGCTTTTCGTTGGTGGTGAATGGGCGAG 4689
Db 1443 GCTTCCATCCGAGTACGCTGCTCGATGCGATGCTTTTCGTTGGTGGTGAATGGGCGAG 1502
QY 4690 GTAGCCGATCAAGCGTATGCAAGCGCGCATTTGCATCAGCCATGATGGATATCTTCTCG 4749
Db 1503 GTAGCCGATCAAGCGTATGCAAGCGCGCATTTGCATCAGCCATGATGGATATCTTCTCG 1562
QY 4750 GCAGGAGCAAGGTGAGATGACAGAGATCTGCGCCGCGCACTTCGCCCAATAGCAGCCAG 4809
Db 1563 GCAGGAGCAAGGTGAGATGACAGAGATCTGCGCCGCGCACTTCGCCCAATAGCAGCCAG 1622
QY 4810 TCCCTTCCGCTTCAGTGACAAAGTGCAGACAGCTGCGCAAGGAACGCCCGCTGTTGGCC 4869
Db 1623 TCCCTTCCGCTTCAGTGACAAAGTGCAGACAGCTGCGCAAGGAACGCCCGCTGTTGGCC 1682
QY 4870 AGCCAGATAGCGCGCTGCTGCTCGAGTTCAATCAGGCGACCGGACAGCTCGGTC 4929
Db 1683 AGCCAGATAGCGCGCTGCTGCTCGAGTTCAATCAGGCGACCGGACAGCTCGGTC 1742
QY 4930 TTGACAAAAGAAACCGGGCGCCCTCGCTGACAGCGGAAACAGCGCGCATCAGAGCAG 4989
Db 1743 TTGACAAAAGAAACCGGGCGCCCTCGCTGACAGCGGAAACAGCGCGCATCAGAGCAG 1802
QY 4990 CCGATTGTCTGTTGTGCCAGTCAATAGCCGAAATAGCCTCTCCACCCAAAGCGCGGAGAA 5049
Db 1803 CCGATTGTCTGTTGTGCCAGTCAATAGCCGAAATAGCCTCTCCACCCAAAGCGCGGAGAA 1862
QY 5050 CTTGCGTGCATCAATCTTGTTCATCATCGGAAACGATCCTCATCTCTGTCTCTTGATCA 5109
Db 1863 CTTGCGTGCATCAATCTTGTTCATCATCGGAAACGATCCTCATCTCTGTCTCTTGATCA 1922
QY 5110 GATCTTTGATCCCTGCGCCATCAGATCTTTGGCGCAAGAAAGCCATCCAGTTTACTTTG 5169
Db 1923 GATCTTTGATCCCTGCGCCATCAGATCTTTGGCGCAAGAAAGCCATCCAGTTTACTTTG 1982
QY 5170 CAGGGCTTCCAAACCTTACAGAGGCGCCCGAGCTGGCAATTCGCGTTTCGTTGCTGTC 5229
Db 1983 CAGGGCTTCCAAACCTTACAGAGGCGCCCGAGCTGGCAATTCGCGTTTCGTTGCTGTC 2042
QY 5230 CATAAACCGCCAGCTAGCAACTGTTGGGAAGGCGATCGGTCGCGGCTCTTCGCTA 5289
Db 2043 CATAAACCGCCAGCTAGCAACTGTTGGGAAGGCGATCGGTCGCGGCTCTTCGCTA 2102
QY 5290 TTAACGCGAGCTGCGCAAGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAAACGCCAGGG 5349
Db 2103 TTAACGCGAGCTGCGCAAGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAAACGCCAGGG 2162
QY 5350 TTTTCCAGTCAAGAGTTGTAATAAAGCAGCGCGAGTGAATGTTGAATACGATCACTATAG 5409
Db 2163 TTTTCCAGTCAAGAGTTGTAATAAAGCAGCGCGAGTGAATGTTGAATACGATCACTATAG 2222
QY 5410 GCGAATTTGAGCT 5423
Db 2223 GCGAATTTGAGCT 2236

RESULT 4
US-10-798-896-2
; Sequence 2, Application US/10798896
; Publication No. US20050238624A1
; GENERAL INFORMATION:
; APPLICANT: ADVISYS, Inc.
; TITLE OF INVENTION: Insulin-Like Growth Factor ("IGF-I") Plasmid Mediated Supplementa
; FILE REFERENCE: 108328.00172 - AVSI-0034
; CURRENT APPLICATION NUMBER: US/10/798,896
; CURRENT FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 3803
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Nucleic acid sequence for the pAV2002 plasmid.
US-10-798-896-2

Query Match 40.9%; Score 2218; DB 9; Length 3803;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2224; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 3190 GAGCCAGGGAACAGCTCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCG 3249
DB 1570 GAGGGGGGGCCGGTACCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCG 1629
QY 3250 TAATCATGTGCATAGCTGTTTCCTGTGTGAATTTATCCGCTCACAATTCACACAAC 3309
DB 1630 TAATCATGTGCATAGCTGTTTCCTGTGTGAATTTATCCGCTCACAATTCACACAAC 1689
QY 3310 ATACGAGCCGGAAGATAAGTGTAAAGCTGGGGTGCCTAAATGAGTGAGCTAACTCACA 3369
DB 1690 ATACGAGCCGGAAGATAAGTGTAAAGCTGGGGTGCCTAAATGAGTGAGCTAACTCACA 1749
QY 3370 TTAATTTGCGTTGCGCTCACTGCCCGCTTTCAGTTCGGGAACCTGTCGTGCCAGCTGCAT 3429
DB 1750 TTAATTTGCGTTGCGCTCACTGCCCGCTTTCAGTTCGGGAACCTGTCGTGCCAGCTGCAT 1809
QY 3430 TAATGAATCGGCCAAGCGGGGGAGAGGGCGTTTGGTATTTGGGGCGCTCTTCGGCTTCC 3489
DB 1810 TAATGAATCGGCCAAGCGGGGGAGAGGGCGTTTGGTATTTGGGGCGCTCTTCGGCTTCC 1869
QY 3490 TCCTCACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3549
DB 1870 TCCTCACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1929
QY 3550 AAGCGGTTAATACGGTTTATCCAGAAATCAGGGGATAACCGAGGAAGAAACATGTGAGCA 3609
DB 1930 AAGCGGTTAATACGGTTTATCCAGAAATCAGGGGATAACCGAGGAAGAAACATGTGAGCA 1989
QY 3610 AAAGGCGAGAAAGCGCAGGAACCGTAAAGGCGCGCTTGTGCTGGGCTTTTTCATAGG 3669
DB 1990 AAAGGCGAGAAAGGCGCAGGAACCGTAAAGGCGCGCTTGTGCTGGGCTTTTTCATAGG 2049
QY 3670 CTCGGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAACCCTG 3729
DB 2050 CTCGGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAACCCTG 2109
QY 3730 ACAGGACTATAAAGATACCAAGGGCTTTCCCTCTGGAAGCTCCCTCGTGGCTCTCTCTGTT 3789
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QY 3790 CCGACCTTCCGCTTACCGGATACCTGTCGCTTTCCTGCTTTCCTTCCGGAAGCGTGGCGCTT 3849
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QY 3910 TGTGTGCAAGAAACCCCGCTTTCAGCCCGACCGCTGCGCTTATCCCGTAATATCGTCTT 3969
DB 2290 TGTGTGCAAGAAACCCCGCTTTCAGCCCGACCGCTGCGCTTATCCCGTAATATCGTCTT 2349
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DB 2350 GAGTCCAAACCCGTTAGACACGACTTATCGCCACTGCGACGACGACCTGCTACAGGATT 2409
QY 4030 AGCAGAGCAGGTATGTAGCGGTGCTACAGAGTCTTCTGAAGTGGTGGCCCTAACTACGGC 4089
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QY 4150 AGAGTTGGTAGCTCTTGATCCGCAACAAACCCAGCTGGTGAAGCTGGTGGTGGTGGT 4209
DB 2530 AGAGTTGGTAGCTCTTGATCCGCAACAAACCCAGCTGGTGAAGCTGGTGGTGGTGGTGGT 2589
QY 4210 TGCAAGCAGCAGATTACGCGCAGAAAAAAGAGATCTCAAGAAAGATCTTCTTGATCTTTCT 4269
DB 2590 TGCAAGCAGCAGATTACGCGCAGAAAAAAGAGATCTCAAGAAAGATCTTCTTGATCTTTCT 2649
QY 4270 ACGGGTCTGACGCTCAGAAAGAACTCGTCAAGAAAGCGATAGAAAGCGATGCGCTCGAA 4329
DB 2650 ACGGGTCTGACGCTCAGAAAGAACTCGTCAAGAAAGCGATAGAAAGCGATGCGCTCGAA 2709
QY 4330 TCGGAGCGCGGATACCGTAAAGCAGGAGAGCGGTCAAGCCATTCGCGCCGCAAGCTCT 4389
DB 2710 TCGGAGCGCGGATACCGTAAAGCAGGAGAGCGGTCAAGCCATTCGCGCCGCAAGCTCT 2769
QY 4390 TCAGCAATATACGCGTAGCAACGCTATGCTCTGATAGCGGTCCGCAACACCCAGCCGG 4449
DB 2770 TCAGCAATATACGCGTAGCAACGCTATGCTCTGATAGCGGTCCGCAACACCCAGCCGG 2829
QY 4450 CCACAGTCGATGATTCAGAAAGCGGCGCATTTTCCACCATGATATTCGCGCAAGCAGGCA 4509
DB 2830 CCACAGTCGATGATTCAGAAAGCGGCGCATTTTCCACCATGATATTCGCGCAAGCAGGCA 2889
QY 4510 TCGCATGGTTCAGCAGAGATCCTCGCGTGGGCAATCGCGCTTGAGCCTGGCGAAC 4569
DB 2890 TCGCATGGTTCAGCAGAGATCCTCGCGTGGGCAATCGCGCTTGAGCCTGGCGAAC 2949
QY 4570 AGTTCCGCTGGCGAGCGCCCTGATGCTCTTCTGTCAGATCATCTCTGATCGAAGACCG 4629
DB 2950 AGTTCCGCTGGCGAGCGCCCTGATGCTCTTCTGTCAGATCATCTCTGATCGAAGACCG 3009
QY 4630 GCTTCCATCCGAGTACGCTGCTCGATGCGATGTTTGGTGGTGGTGGTGGTGGTGGTGGT 4689
DB 3010 GCTTCCATCCGAGTACGCTGCTCGATGCGATGTTTGGTGGTGGTGGTGGTGGTGGTGGT 3069
QY 4690 GTAGCCGATCAAGCGTATGACCGCGCGCATTCGATCAGCCATGATGATCTTTCTCG 4749
DB 3070 GTAGCCGATCAAGCGTATGACCGCGCGCATTCGATCAGCCATGATGATCTTTCTCG 3129
QY 4750 GCAGGAGCAAGGTGAGATGACAGGAGATCTGCGCCGCGCATTCGCGCCATAGCAGCCAG 4809
DB 3130 GCAGGAGCAAGGTGAGATGACAGGAGATCTGCGCCGCGCATTCGCGCCATAGCAGCCAG 3189
QY 4810 TCCCTTCCCGCTTCACTGACAAAGTTCGAGCAGCAGCTGCGCAAGAAACGCGCTGCTGGCC 4869
DB 3190 TCCCTTCCCGCTTCACTGACAAAGTTCGAGCAGCAGCTGCGCAAGAAACGCGCTGCTGGCC 3249
QY 4870 AGCCAGATAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4929
DB 3250 AGCCAGATAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3309
QY 4930 TTGACAAAAAGAAACCGGGCGCCCTGCGCTGACAGCGGAAACACAGCGCGCATCAGAGCAG 4989
DB 3310 TTGACAAAAAGAAACCGGGCGCCCTGCGCTGACAGCGGAAACACAGCGCGCATCAGAGCAG 3369
QY 4990 CCGATTGTCTGTTGTCGCCAGTCAATAGCCGAATAGCTCTTCCACCAAGCGCGCGAGAA 5049

Db 3370 CCAGTGTCTGTTGGCCAGTCATAGCCGAAATAGCTCTCCACCCAGCGCGGAGAA 3429
QY 5050 CTGCGGTGCAATCACTTGTTCATCATCGAAGCATCTCATCTGTCTCTTGATCA 5109
Db 3430 CTGCGGTGCAATCACTTGTTCATCATCGAAGCATCTCATCTGTCTCTTGATCA 3489
QY 5110 GATCTTGATCCCTGGCCATCAGATCTTGGCGGCAAGAACCCATCCAGTTTACTTTG 5169
Db 3490 GATCTTGATCCCTGGCCATCAGATCTTGGCGGCAAGAACCCATCCAGTTTACTTTG 3549
QY 5170 CAGGGCTTCCCAACTTACAGAGGGGCCCCAGCTGGCAATTCGGTTCGCTGTCTGTC 5229
Db 3550 CAGGGCTTCCCAACTTACAGAGGGGCCCCAGCTGGCAATTCGGTTCGCTGTCTGTC 3609
QY 5230 CATAAACCCGCCAGTCTAGCACTGTTGGGAAGGGCGATCGGTGCGGGCTCTCTGCGTA 5289
Db 3610 CATAAACCCGCCAGTCTAGCACTGTTGGGAAGGGCGATCGGTGCGGGCTCTCTGCGTA 3669
QY 5290 TTAGCCAGCTGGCAAGGGGATGCTGCAAGGCGATTAGTTGGGTAAAGCCAGGG 5349
Db 3670 TTAGCCAGCTGGCAAGGGGATGCTGCAAGGCGATTAGTTGGGTAAAGCCAGGG 3729
QY 5350 TTTTCCAGTCAAGACCTTGTAAACCGACGCCAGTGAATTTGTAATACGACTCACTATAG 5409
Db 3730 TTTTCCAGTCAAGACCTTGTAAACCGACGCCAGTGAATTTGTAATACGACTCACTATAG 3789
QY 5410 GCGCAATTGGAGCT 5423
Db 3790 GCGCAATTGGAGCT 3803

RESULT 5

US-09-861-101-2
; Sequence 2, Application US/09861101
; Publication No. US20030018984A1
; GENERAL INFORMATION:
; APPLICANT: COLEMAN, MICHAEL
; SCHWARTZ, ROBERT
; DEMAYO, FRANCESCO J.
; TITLE OF INVENTION: IGF-1 EXPRESSION SYSTEM AND
; METHODS OF USE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: PASCSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/861.101
; FILING DATE: 18-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,572
; FILING DATE: November 19, 1997
; APPLICATION NUMBER: 60/031,539
; FILING DATE: December 2, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/185-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440

; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3600 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-861-101-2

Query Match 40.9%; Score 2215.8; DB 3; Length 3600;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3205 CTGAGCTTTTGTCCCTTTAGTCAGGGTTAAATTCGAGCTTGGCGTAAATCATGTCATAG 3264
Db 19 CCAGAGCTTTTGTTCCTTTAGTAGAGGGTTAAATTCGAGCTTGGCGTAAATCATGTCATAG 78
QY 3265 CTGTTTCTCTGTGAAATTTGTTATCCGCTCACAAATTCACACAAATACGAGCCGGAAGC 3324
Db 79 CTGTTTCTCTGTGAAATTTGTTATCCGCTCACAAATTCACACAAATACGAGCCGGAAGC 138
QY 3325 ATAAAGTGTAAAGCTCGGGTGCTTAATAGTGTAGCTAACTCACATTAATTGCGTTGCGC 3384
Db 139 ATAAAGTGTAAAGCTCGGGTGCTTAATAGTGTAGCTAACTCACATTAATTGCGTTGCGC 198
QY 3385 TCACTGCCCGCTTTCAGTCCGGAACCTGTGCGGAGCTGATTAATGAATCGGCCAA 3444
Db 199 TCACTGCCCGCTTTCAGTCCGGAACCTGTGCGGAGCTGATTAATGAATCGGCCAA 258
QY 3445 CGCGCGGGAGAGCGGTTTGGCTATTGGCGCTCTTCCGCTTCTCCGCTCACTGACTCG 3504
Db 259 CGCGCGGGAGAGCGGTTTGGCTATTGGCGCTCTTCCGCTTCTCCGCTCACTGACTCG 318
QY 3505 CTGCGCTCGGTCGTTCCGCTGCGGCGAGCGGTATCAGTCACTCAAAAGCGGTAAATACGG 3564
Db 319 CTGCGCTCGGTCGTTCCGCTGCGGCGAGCGGTATCAGTCACTCAAAAGCGGTAAATACGG 378
QY 3565 TTATCCACAGAAATCAGGGGTAACGAGGAAGCAATGTGAGCAAAAGCCGCAAAAG 3624
Db 379 TTATCCACAGAAATCAGGGGTAACGAGGAAGCAATGTGAGCAAAAGCCGCAAAAG 438
QY 3625 GCAGGAACCGTAAAGGCGCGTGTCTGCGCTTTTCCATAGGCTCCGCCCTGAC 3684
Db 439 GCAGGAACCGTAAAGGCGCGTGTCTGCGCTTTTCCATAGGCTCCGCCCTGAC 498
QY 3685 GAGCATCAAAAATCGACGCTCAAGTCAAGTGTGGGAAACCCGACAGGACTATAAGA 3744
Db 499 GAGCATCAAAAATCGACGCTCAAGTCAAGTGTGGGAAACCCGACAGGACTATAAGA 558
QY 3745 TACGAGCGTTTCCCGTGGAAAGCTCCCTGCGGCTCTCTGTTCCGACCCCTGCCGCTT 3804
Db 559 TACGAGCGTTTCCCGTGGAAAGCTCCCTGCGGCTCTCTGTTCCGACCCCTGCCGCTT 618
QY 3805 ACCGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTCTCTAGTCTACGC 3864
Db 619 ACCGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTCTCTAGTCTACGC 678
QY 3865 TGTAGGTATCTCAGTTCCGTTGAGGTGCTTCCGCTTCCGCTGCGGCTGTGTGACGAACCC 3924
Db 679 TGTAGGTATCTCAGTTCCGTTGAGGTGCTTCCGCTTCCGCTGCGGCTGTGTGACGAACCC 738
QY 3925 CCGTTTCAGCCCGACCGCTTATCCGTTATCCGTTATCTGTTAGTCCAAACCCGTA 3984
Db 739 CCGTTTCAGCCCGACCGCTTATCCGTTATCCGTTATCTGTTAGTCCAAACCCGTA 798
QY 3985 AGACACGACTTATCGCCACTGGCAGCAGCCACTGTTAAAGGATTAGCAGAGCGAGTAT 4044
Db 799 AGACACGACTTATCGCCACTGGCAGCAGCCACTGTTAAAGGATTAGCAGAGCGAGTAT 858
QY 4045 GTAGGCGGTGCTACAGAGTTCTTGAAGTGTGGCTTAATCAGGCTACACTAGGAAGACA 4104
Db 859 GTAGGCGGTGCTACAGAGTTCTTGAAGTGTGGCTTAATCAGGCTACACTAGGAAGACA 918

QY 4105 GTATTGGTATCTGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGAGTTGGTAGCTCT 4164
DB 919 GTATTGGTATCTGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGAGTTGGTAGCTCT 978
QY 4165 TGNATCGGCAAAACAAACACCGCTGCTAGCGGTGGTATTTTGTTCGAAGCAGAGATT 4224
DB 979 TGNATCGGCAAAACAAACACCGCTGCTAGCGGTGGTATTTTGTTCGAAGCAGAGATT 1038
QY 4225 ACAGCAGAAAAAGAGATCTCAAGAGATCTTTTGTATCTTTTCTACGGGCTCTGACGCT 4284
DB 1039 ACAGCAGAAAAAGAGATCTCAAGAGATCTTTTGTATCTTTTCTACGGGCTCTGACGCT 1098
QY 4285 CAGAAAGACTCTCAAGAGAGGATGAAGGCGATCGCTGCGAATCGGAGCGGCGATA 4344
DB 1099 CAGAAAGACTCTCAAGAGAGGATGAAGGCGATCGCTGCGAATCGGAGCGGCGATA 1158
QY 4345 CCGTAAGCAGAGGAGCGGTGAGCCCATTCGCGCCAGCTCTTCAGCAATATCACGG 4404
DB 1159 CCGTAAGCAGAGGAGCGGTGAGCCCATTCGCGCCAGCTCTTCAGCAATATCACGG 1218
QY 4405 GTAGCAACGCTATGCTCTGATAGCGGTGCGCCACACCGCGGCCACAGTCGATGAAT 4464
DB 1219 GTAGCAACGCTATGCTCTGATAGCGGTGCGCCACACCGCGGCCACAGTCGATGAAT 1278
QY 4465 CCAGAAAAAGCGCCATTTTCCACCATGATATTCGCAAGCAGGCATCGCCATGGGTCAAG 4524
DB 1279 CCAGAAAAAGCGCCATTTTCCACCATGATATTCGCAAGCAGGCATCGCCATGGGTCAAG 1338
QY 4525 ACAGATCTCTCGCGCTGCGGCGATGCGGCTTGAGCTGCGCAACAGTTGCGGCTGGCGG 4584
DB 1339 ACAGATCTCTCGCGCTGCGGCGATGCGGCTTGAGCTGCGCAACAGTTGCGGCTGGCGG 1398
QY 4585 AGCCCTGATGCTCTTCGCTCCAGATCATCTGATCGACAGACCGGCTTCCATCCAGTA 4644
DB 1399 AGCCCTGATGCTCTTCGCTCCAGATCATCTGATCGACAGACCGGCTTCCATCCAGTA 1458
QY 4645 CGTGCTCGCTCGATGCGGATGTTTCGCTGCTGATGCGAATGGGCGAGTAGCGGATCAAGC 4704
DB 1459 CGTGCTCGCTCGATGCGGATGTTTCGCTGCTGATGCGAATGGGCGAGTAGCGGATCAAGC 1518
QY 4705 GTATGAGCGCGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4764
DB 1519 GTATGAGCGCGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1578
QY 4765 GATGACAGAGATCTGCGCCGCGCATGATGATGATGATGATGATGATGATGATGATGATGAT 4824
DB 1579 GATGACAGAGATCTGCGCCGCGCATGATGATGATGATGATGATGATGATGATGATGATGAT 1638
QY 4825 GTGACAACTGACGACAGCTGCGCAAGGAACGCGCGTGTGGCGAGCCACGATAGCCGC 4884
DB 1639 GTGACAACTGACGACAGCTGCGCAAGGAACGCGCGTGTGGCGAGCCACGATAGCCGC 1698
QY 4885 GGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4944
DB 1699 GGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1758
QY 4945 GGGCGCCCTGCGCTGACAGCCGGAACACGCGGCGATCAGAGCAGCCGATGCTGCTGCT 5004
DB 1759 GGGCGCCCTGCGCTGACAGCCGGAACACGCGGCGATCAGAGCAGCCGATGCTGCTGCT 1818
QY 5005 GCCAGTCTAGCCGAATAGCTCTCCACCAAGCGCGCGGAACCTGCTGCAATCA 5064
DB 1819 GCCAGTCTAGCCGAATAGCTCTCCACCAAGCGCGCGGAACCTGCTGCAATCA 1878
QY 5065 TCTTGTTCATATGCGAAACGATCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCT 5124
DB 1879 TCTTGTTCATATGCGAAACGATCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCT 1938
QY 5125 CGCCATCAGATCTTGGCGCAAGAAAGCATCCAGTTTACTTTTGTGAGGGCTTCCCAACC 5184
DB 1939 CGCCATCAGATCTTGGCGCAAGAAAGCATCCAGTTTACTTTTGTGAGGGCTTCCCAACC 1998

QY 5185 TTACCAAGAGGCGCCCAAGCTGCAATTCGGTTCCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5244
DB 1999 TTACCAAGAGGCGCCCAAGCTGCAATTCGGTTCCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2058
QY 5245 TCTAGCAACTGTTGGGAAGGCGATCGGTGCGGCGCTCTTCGCTATATACGCCAGCTGGCG 5304
DB 2059 TCTAGCAACTGTTGGGAAGGCGATCGGTGCGGCGCTCTTCGCTATATACGCCAGCTGGCG 2118
QY 5305 AAAGGGGATGCTGCTCAAGGCGATTAAAGTTGGGTAAACGCCAGGCTTTTCCAGTACCA 5364
DB 2119 AAAGGGGATGCTGCTCAAGGCGATTAAAGTTGGGTAAACGCCAGGCTTTTCCAGTACCA 2178
QY 5365 CGTTGTAAACGACGCGCCAGTGAATTTGTAATACGACTCACTATAGGCGGAATTTGGAGCT 5423
DB 2179 CGTTGTAAACGACGCGCCAGTGAATTTGTAATACGACTCACTATAGGCGGAATTTGGAGCT 2237

RESULT 6
US-10-281-067B-26
; Sequence 26, Application US/10281067B
; Publication No. US20040138111A1
; GENERAL INFORMATION:
; APPLICANT: Baylor College of Medicine
; TITLE OF INVENTION: A COMPOSITION AND METHOD TO ALTER LEAN BODY MASS AND BOND PROPERT
; FILE REFERENCE: 108328.00071 - AVSI-0008
; CURRENT APPLICATION NUMBER: US/10/281,067B
; CURRENT FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 26
; LENGTH: 3558
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence for the inducible pGR1774 containing GHRH.
US-10-281-067B-26

Query Match 40.8%; Score 2211.6; DB 7; Length 3558;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2217; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3190 GAGCCAGGCAACAGCTCAGCTTTTGTTCCTTTTAGTGAGGGTTAATTTGAGCTTTGGCG 3249
DB 1200 GAGGGGGCGCCGTACAGCTTTTGTTCCTTTTAGTGAGGGTTAATTTGAGCTTTGGCG 1259
QY 3250 TAAATCATGCTAGCTGTTTCTGTTGAAATTTGTTATCCGCTCAATTTCCACAAAC 3309
DB 1260 TAAATCATGCTAGCTGTTTCTGTTGAAATTTGTTATCCGCTCAATTTCCACAAAC 1319
QY 3310 ATACGAGCGGAAGCATAAAGTGTAAAGCTCGGGTGCCTTAATGAGTGAGCTAACTCACA 3369
DB 1320 ATACGAGCGGAAGCATAAAGTGTAAAGCTCGGGTGCCTTAATGAGTGAGCTAACTCACA 1379
QY 3370 TTAATTTGCTTGGCTCACTGCGCTTTCAGTTCGGGAAACCTGTCGTCGCAAGCTGCAT 3429
DB 1380 TTAATTTGCTTGGCTCACTGCGCTTTCAGTTCGGGAAACCTGTCGTCGCAAGCTGCAT 1439
QY 3430 TAAATGAATCGGCAACGCGCGGGAGAGCGGTTTTCGTTATTTGGGCGCTCTTCCGCTTCC 3489
DB 1440 TAAATGAATCGGCAACGCGCGGGAGAGCGGTTTTCGTTATTTGGGCGCTCTTCCGCTTCC 1499
QY 3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTTCGCTGCGGGAGCGGTATCAGCTCACTCA 3549
DB 1500 TCGCTCACTGACTCGCTGCGCTCGGTCGTTTCGCTGCGGGAGCGGTATCAGCTCACTCA 1559
QY 3550 AAAGGCGTAAATACGGTTATCCAGAAATCAGGGGATAACGCAAGAAAGAAACATGTGAGCA 3609
DB 1560 AAAGGCGTAAATACGGTTATCCAGAAATCAGGGGATAACGCAAGAAAGAAACATGTGAGCA 1619
QY 3610 AAAGGCGCAAAAGCCAGGAACCGTAAAAAGGCGCGCTTGTGCGGTTTTCCTATAGG 3669
DB 1620 AAAGGCGCAAAAGCCAGGAACCGTAAAAAGGCGCGCTTGTGCGGTTTTCCTATAGG 1679

QY 3670 CTCGCGCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
Db 1680 CTCGCGCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 1739
QY 3730 ACAGGACTATAAGATACACAGCGGTTTCCCGCTGGAGCTCCCTCGTGGCTCTCTCTGT 3789
Db 1740 ACAGGACTATAAGATACACAGCGGTTTCCCGCTGGAGCTCCCTCGTGGCTCTCTCTGT 1799
QY 3790 CGACCCCTGCGCTTACCGGATACCTGTGCGCCTTTCTCCCTTGGGAAGCGTGGCGCTT 3849
Db 1800 CGACCCCTGCGCTTACCGGATACCTGTGCGCCTTTCTCCCTTGGGAAGCGTGGCGCTT 1859
QY 3850 TCTCATAGCTACCGCTGTAGGTATCTCAGTTCGGTGTAGGTCTGCTCCCAAGCTGGGC 3909
Db 1860 TCTCATAGCTACCGCTGTAGGTATCTCAGTTCGGTGTAGGTCTGCTCCCAAGCTGGGC 1919
QY 3910 TGTGTGACGAACCCCGCTTACGCGCCGACCGCTGGCGCTTATCCCGTAACTATCGTCTT 3969
Db 1920 TGTGTGACGAACCCCGCTTACGCGCCGACCGCTGGCGCTTATCCCGTAACTATCGTCTT 1979
QY 3970 GAGTCCAAACCCGCTAAGACACGACTTATCGCCACTGGCAGACGCCACTGGTAAACAGATT 4029
Db 1980 GAGTCCAAACCCGCTAAGACACGACTTATCGCCACTGGCAGACGCCACTGGTAAACAGATT 2039
QY 4030 AGCAGACGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCTTAAGTACGGC 4089
Db 2040 AGCAGACGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCTTAAGTACGGC 2099
QY 4090 TACACTAGAAGAACAGTATTTGTTATCTGCGCTCTGCTGAAGCCAGTGTACTTTGGGAAA 4149
Db 2100 TACACTAGAAGAACAGTATTTGTTATCTGCGCTCTGCTGAAGCCAGTGTACTTTGGGAAA 2159
QY 4150 AGAGTTGGTAGCTCTTGATCCGCAACAAACCAACCGCTGGTAGCGGTGGTTTTTGTGTT 4209
Db 2160 AGAGTTGGTAGCTCTTGATCCGCAACAAACCAACCGCTGGTAGCGGTGGTTTTTGTGTT 2219
QY 4210 TGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAGATCTTTGATCTTTCT 4269
Db 2220 TGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAGATCTTTGATCTTTCT 2279
QY 4270 ACCGGGTCTCAGCTCAGAGAACTCGTCAAGAGGCGATAGAGGCGATCGCGTCGAA 4329
Db 2280 ACCGGGTCTCAGCTCAGAGAACTCGTCAAGAGGCGATAGAGGCGATCGCGTCGAA 2339
QY 4330 TCGGAGCGCGGATACCGTAAAGCAGAGGAGCGGTACGCCATTCGCGCCCAAGCTCT 4389
Db 2340 TCGGAGCGCGGATACCGTAAAGCAGAGGAGCGGTACGCCATTCGCGCCCAAGCTCT 2399
QY 4390 TCAGCAATATACGGGTAGCCAAAGCTATGCTGTATAGCGGTCCGCGCACACCCAGCGG 4449
Db 2400 TCAGCAATATACGGGTAGCCAAAGCTATGCTGTATAGCGGTCCGCGCACACCCAGCGG 2459
QY 4450 CCACAGTCGATGAATCAGAAAGCGGCCATTTTCCACCATGATATTTCCGCAAGCAGGCA 4509
Db 2460 CCACAGTCGATGAATCAGAAAGCGGCCATTTTCCACCATGATATTTCCGCAAGCAGGCA 2519
QY 4510 TCGCCATGGGTACAGCAGAGATCTTCGCGCTCGGGCATGCGCGCTTGGCCTGGCGAAC 4569
Db 2520 TCGCCATGGGTACAGCAGAGATCTTCGCGCTCGGGCATGCGCGCTTGGCCTGGCGAAC 2579
QY 4570 AGTTTCGCTGGCGGAGCCCTGATGCTCTTCGTCAGATCATCTGATCGACAGACCG 4629
Db 2580 AGTTTCGCTGGCGGAGCCCTGATGCTCTTCGTCAGATCATCTGATCGACAGACCG 2639
QY 4630 GCTTCATCCGAGTACGCTGCTCGCTCGATGCGATGTTTCGTTGGTGGTGGGCGAG 4689
Db 2640 GCTTCATCCGAGTACGCTGCTCGCTCGATGCGATGTTTCGTTGGTGGTGGGCGAG 2699
QY 4690 GTAGCCGGATCAAGCGTATGACGCGCGGATTCGATCAGCAGATGATGATCTTTCTCG 4749
Db 2700 GTAGCCGGATCAAGCGTATGACGCGCGGATTCGATCAGCAGATGATGATCTTTCTCG 2759

QY 4750 GCAGGAGCAAGGTGAGATGACAGGAGATCTTCCCGGCACTTTCGCCAATAGCAGCCAG 4809
Db 2760 GCAGGAGCAAGGTGAGATGACAGGAGATCTTCCCGGCACTTTCGCCAATAGCAGCCAG 2819
QY 4810 TCCCTTCGCGCTTCAAGTGAACAAGTCAGACAGCTGCGCAAGGAACGCCCTGCTGGCC 4869
Db 2820 TCCCTTCGCGCTTCAAGTGAACAAGTCAGACAGCTGCGCAAGGAACGCCCTGCTGGCC 2879
QY 4870 AGCCAGTAGCGCGCTGCTGCTCCTCAGTTCATTCAGGCGCACCGGACAGGTGCGTC 4929
Db 2880 AGCCAGTAGCGCGCTGCTGCTCCTCAGTTCATTCAGGCGCACCGGACAGGTGCGTC 2939
QY 4930 TTGACAAAAAAGAACCCGGGCGCCCTCGCTGACAGCGGAACACGCGCGCATCAGAGCAG 4989
Db 2940 TTGACAAAAAAGAACCCGGGCGCCCTCGCTGACAGCGGAACACGCGCGCATCAGAGCAG 2999
QY 4990 CGGATTGTCTGTTGTGCCAGTCATAGCGAATAGCTCTCCACCCAAAGCGCGGAGAA 5049
Db 3000 CGGATTGTCTGTTGTGCCAGTCATAGCGAATAGCTCTCCACCCAAAGCGCGGAGAA 3059
QY 5050 CTTGCGTGAATCCATCTTTTCAATCATGCGAAACGATCCTCCTCTCTTGATCA 5109
Db 3060 CTTGCGTGAATCCATCTTTTCAATCATGCGAAACGATCCTCCTCTCTTGATCA 3119
QY 5110 GATCTTTGATCCCTGCGCCATCAGATCTTTGGCGCAAGAAAGCCATCCAGTTTACTTTG 5169
Db 3120 GATCTTTGATCCCTGCGCCATCAGATCTTTGGCGCAAGAAAGCCATCCAGTTTACTTTG 3179
QY 5170 CAGGGCTTCCCAACCTTACAGAGGCGGCCCGCAGCTGGCAATTCGCGTTGCTGTGTC 5229
Db 3180 CAGGGCTTCCCAACCTTACAGAGGCGGCCCGCAGCTGGCAATTCGCGTTGCTGTGTC 3239
QY 5230 CATAAAAACCGCCAGTCTAGCACTTTTGGGAGGGGATCGGTGCGGCGCTCTTCGCTA 5289
Db 3240 CATAAAAACCGCCAGTCTAGCACTTTTGGGAGGGGATCGGTGCGGCGCTCTTCGCTA 3299
QY 5290 TTACGCGCAGCTGGCGAAAGGGGATGCTGCTCAAGCGATTAAGTTGGGTAAACGCCAGG 5349
Db 3300 TTACGCGCAGCTGGCGAAAGGGGATGCTGCTCAAGCGATTAAGTTGGGTAAACGCCAGG 3359
QY 5350 TTTTCCAGTCACGAGCTTTGTAACACGCGGCGAGTGAATTTGTAATACGACTATATAG 5409
Db 3360 TTTTCCAGTCACGAGCTTTGTAACACGCGGCGAGTGAATTTGTAATACGACTATATAG 3419
QY 5410 GCGCAATT 5417
Db 3420 GCGCAATT 3427

RESULT 7
US-10-764-818A-26
; Sequence 26, Application US/10764818A
; Publication No. US20040204358A1
; GENERAL INFORMATION:
; APPLICANT: ADVISYS
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES
; TITLE OF INVENTION: CULLING IN HERD ANIMALS
; FILE REFERENCE: 108328.00170 - AVSI-0033
; CURRENT APPLICATION NUMBER: US/10/764, 818A
; CURRENT FILING DATE: 2004-01-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 3558
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence for the inducible pGR1774 with human GHRH
US-10-764-818A-26
Query Match 40.8%; Score 2211.6; DB 8; Length 3558;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2217; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Db 3360 TTTTCCAGTCACGAGCTTGTAAACGAGCGCCAGTGAATTGTATACGACTCACTATAG 3419
Qy 5410 GCGCAATT 5417
Db 3420 GCGCAATT 3427

RESULT 8

US-10-021-403A-10
; Sequence 10, Application US/10021403A
; Publication No. US20030074679A1
; GENERAL INFORMATION:
; APPLICANT: Advise
; TITLE OF INVENTION: Administration of Nucleic Acid Sequence to Female Animal to Enhance
; TITLE OF INVENTION: Growth in Offspring
; FILE REFERENCE: HO-P0201USI/100021476/OTA 00-91
; CURRENT APPLICATION NUMBER: US/10/021.403A
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/255,021
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 2192
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is a plasmid vector comprising a pVC0289 backbone
US-10-021-403A-10

Query Match 39.8%; Score 2160; DB 5; Length 2192;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2166; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 3190 GAGCCAGCGAACAGCTCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCG 3249
Db 17 GAGGGGGGGCCGGTACCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCG 76
Qy 3250 TAATCATGGTCATAGCTGTTTCTGTGTGAAATTTGTTATTCGGCTCACAATTCACACAAC 3309
Db 77 TAATCATGGTCATAGCTGTTTCTGTGTGAAATTTGTTATTCGGCTCACAATTCACACAAC 136
Qy 3310 ATACGACCGGAGCATAAAGCTGTAAGCTGGGGTCCCTAAATGAGTGAGTCACTCA 3369
Db 137 ATACGACCGGAGCATAAAGCTGTAAGCTGGGGTCCCTAAATGAGTGAGTCACTCA 196
Qy 3370 TTAATTCGGTTGCGCTCACTGCGCGCTTTCAGTTCGGGAAACCTGTGTCGCGACTGCAT 3429
Db 197 TTAATTCGGTTGCGCTCACTGCGCGCTTTCAGTTCGGGAAACCTGTGTCGCGACTGCAT 256
Qy 3430 TAATGAATTCGGCCAAACGCGGGGAGAGGGGGTTTGGTATTTGGGGCGCTTTCGCGTTCC 3489
Db 257 TAATGAATTCGGCCAAACGCGGGGAGAGGGGGTTTGGTATTTGGGGCGCTTTCGCGTTCC 316
Qy 3490 TCGCTCACTGACTCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 3549
Db 317 TCGCTCACTGACTCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 376
Qy 3550 AAGCGCGTAAATACGGTTATCCACAGATCAGGGGATAACCGAGGAAAGAAATCATGTGAGCA 3609
Db 377 AAGCGCGTAAATACGGTTATCCACAGATCAGGGGATAACCGAGGAAAGAAATCATGTGAGCA 436
Qy 3610 AAGCGCGCAAAAGGCGCAGAAACCGTTAAAGCGCGGTTGCTGGGCTTTTCCATAGG 3669
Db 437 AAGCGCGCAAAAGGCGCAGAAACCGTTAAAGCGCGGTTGCTGGGCTTTTCCATAGG 496
Qy 3670 CTCCGCCCTGACGAGCATCAAAAATCGAGCTCAAGTCAGAGGTGCGGAAACCCG 3729
Db 497 CTCCGCCCTGACGAGCATCAAAAATCGAGCTCAAGTCAGAGGTGCGGAAACCCG 556
Qy 3730 ACAGGACTATAAAGATACAGCGCGTTTCCCTCGGAAGCTCCCTCGTGGCTCTCTGTT 3789

Db 557 ACAGGACTATAAAGATACAGCGCGTTTCCCTCGGAAGCTCCCTCGTGCCTCTCTGTT 616
Qy 3790 CCGACCTCGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
Db 617 CCGACCTCGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTT 676
Qy 3850 TCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCTGCTCCAAAGCTGGGC 3909
Db 677 TCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCTGCTCCAAAGCTGGGC 736
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Qy 3970 GAGTCCAAACCCGCTTACGACGACTTATCGCCTGSCACGACCTGCTGTAACAGGATT 4029
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Db 977 AGAGTTGGTAGCTCTTATCCGCAACAAACACCGCTGCTAGCGTGGTTTTTGT 1036
Qy 4210 TGCAAGCAGCAGATTAACGCGCAGAAAAAGGATCTCAAGAGATCTCTTGTATCTTCT 4269
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Qy 4330 TCGGAGCGGATACCGTAAAGCAGGAGAGCGCTCAGCCCATTCGCGCCCAAGCTCT 4389
Db 1157 TCGGAGCGGATACCGTAAAGCAGGAGAGCGCTCAGCCCATTCGCGCCCAAGCTCT 1216
Qy 4390 TCAGCAATATCAGGGTAGCAACGGCTATGCTCTGATAGCGGTCCGCAACCCAGCGG 4449
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Qy 4450 CCACAGTCGATGAATCAGAAAAAGCGGCCATTTTCCACCATGATATTCGCAAGCGCA 4509
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Qy 4570 AGTTTCGCTGCGCGAGCCCTCTGATGCTCTTCTGTCAGATCATCTGATCGCAAGACCG 4629
Db 1397 AGTTTCGCTGCGCGAGCCCTCTGATGCTCTTCTGTCAGATCATCTGATCGCAAGACCG 1456
Qy 4630 GCTTCCATTCGAGTACGCTGCTCGATCGATGGATGTTTTCGTTGGTGGTGAATGGGCG 4689
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Qy 4750 GCAGGACCAAGGTGAGATGACAGGAGATCTTTCGCGCGCATCTTCGCCAATAGCAGCG 4809
Db 1577 GCAGGACCAAGGTGAGATGACAGGAGATCTTTCGCGCGCATCTTCGCCAATAGCAGCG 1636
Qy 4810 TCCCTTCCGCTTCAAGTGAACAGTTCAGGACAGCTGCGGAGGAAACCGCTGCTGCGG 4869
Db 1637 TCCCTTCCGCTTCAAGTGAACAGTTCAGGACAGCTGCGGAGGAAACCGCTGCTGCGG 1696


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Qy 4390 TCAGCAATATACAGGGTAGCAACGCTATGCTCTGATAGCGGTCCGCGCACACAGCCGG 4449
Db 2559 TCAGCAATATACAGGGTAGCAACGCTATGCTCTGATAGCGGTCCGCGCACACAGCCGG 2618
Qy 4450 CCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTTGGCAAGCAGGCA 4509
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Qy 4510 TCGCCATGGGTACGACGAGATCTCCCGCTCGGGCATCGCGCTTGAGCCTGGCGAAC 4569
Db 2679 TCGCCATGGGTACGACGAGATCTCCCGCTCGGGCATCGCGCTTGAGCCTGGCGAAC 2738
Qy 4570 AGTTCCGCTCGCGGAGCCCTCATGCTCTTGGTCCAGATCATCTCATGACACAGACCG 4629
Db 2739 AGTTCCGCTCGCGGAGCCCTCATGCTCTTGGTCCAGATCATCTCATGACACAGACCG 2798
Qy 4630 GCTTCCATCCGAGTACGTCGCTCGCATCGCATGGTTCGTTTGGTGGTTCGAATGGGCAG 4689
Db 2799 GCTTCCATCCGAGTACGTCGCTCGCATCGCATGGTTCGTTTGGTGGTTCGAATGGGCAG 2858
Qy 4690 GTAGCCGGATCAAGCGTATGACGAGCGCGCATTTGCATCAGCCATGATGATCTTTCTCG 4749
Db 2859 GTAGCCGGATCAAGCGTATGACGAGCGCGCATTTGCATCAGCCATGATGATCTTTCTCG 2918
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Qy 5110 GATCTTGATCCCTGCGCCATCAGATCCTTGGCGGCAAGAACGATCCAGTTTACTTTG 5169
Db 3279 GATCTTGATCCCTGCGCCATCAGATCCTTGGCGGCAAGAACGATCCAGTTTACTTTG 3338
Qy 5170 CAGGGCTTCCCACTTACAGAGGGCGCCAGCTGCGCAATTCGGTTCGTTGCTGTC 5229
Db 3339 CAGGGCTTCCCACTTACAGAGGGCGCCAGCTGCGCAATTCGGTTCGTTGCTGTC 3398
Qy 5230 CATAAAACCGCCAGTCTAGCAACTGTGGGAAAGGCGATCGGTGCGGGCTCTTCGCTA 5289
Db 3399 CATAAAACCGCCAGTCTAGCAACTGTGGGAAAGGCGATCGGTGCGGGCTCTTCGCTA 3458
Qy 5290 TTAGCCAGCTGGCGAAGGGGGATGTGCTCAAGGGGATTAAGTTGGGTAACGCCAGGG 5349
Db 3459 TTAGCCAGCTGGCGAAGGGGGATGTGCTCAAGGGGATTAAGTTGGGTAACGCCAGGG 3518
Qy 5350 TTTTCCAGTACACGAC 5365
Db 3519 TTTTCCAGTACACGAC 3534
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RESULT 10
US-10-395-709-11
; Sequence 11, Application US/10395709
; Publication No. US20040014645A1

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; GENERAL INFORMATION:  
; APPLICANT: Advivys  
; TITLE OF INVENTION: INCREASED DELIVERY OF A NUCLEIC ACID CONSTRUCT IN VIVO BY THE POL  
; FILE OF INVENTION: GLUTAMATE ("PLG") SYSTEM  
; CURRENT APPLICATION NUMBER: US/10/395,709  
; CURRENT FILING DATE: 2003-03-24  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 11  
; LENGTH: 3534  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence for the operatively linked components of the HV-GHRH pla  
; OTHER INFORMATION: smid.  
US-10-395-709-11
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Query Match 39.8%; Score 2160; DB 7; Length 3534;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 2166; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
  
Qy 3190 GAGCGAGGGAACAGCTGCTTTTGTCCCTTTAGTGAGGGTTAATTTGAGCTTGGCG 3249  
Db 1359 GAGGGGGGGCCCGGTACCACTTTTGTTCCTTTAGTGAGGGTTAATTTGAGCTTGGCG 1418  
Qy 3250 TAATCATGTGTCATAGCTGTTTCTGTGTGAAATTTTATCCGCTCACAAATTCACACAAAC 3309  
Db 1419 TAATCATGTGTCATAGCTGTTTCTGTGTGAAATTTTATCCGCTCACAAATTCACACAAAC 1478  
Qy 3310 ATACGAGCCGGAAGCAATAAGTGTAAAGCCTGGGGTGCCTTAATGAGTGAGCTAACTCACA 3369  
Db 1479 ATACGAGCCGGAAGCAATAAGTGTAAAGCCTGGGGTGCCTTAATGAGTGAGCTAACTCACA 1538  
Qy 3370 TTAATTGCGTTGCGCTCACTGCGCGCTTTTCAGTTCGCGGAAACCTGTGCGTGCAGCTGCAT 3429  
Db 1539 TTAATTGCGTTGCGCTCACTGCGCGCTTTTCAGTTCGCGGAAACCTGTGCGTGCAGCTGCAT 1598  
Qy 3430 TAATGAATCCGCCAACCGCGGGGAGAGCGGTTTGGTATTTGGCGCTCTTCCGCTTCC 3489  
Db 1599 TAATGAATCCGCCAACCGCGGGGAGAGCGGTTTGGTATTTGGCGCTCTTCCGCTTCC 1658  
Qy 3490 TCGCTCACTGACTCGCTCGCTCGCTCGGTTCGCGTGGCGAGCGGTATCAGCTCACTCA 3549  
Db 1659 TCGCTCACTGACTCGCTCGCTCGGTTCGCGTGGCGAGCGGTATCAGCTCACTCA 1718  
Qy 3550 AAGCGGTAATACGTTTATCCACGAATCAGGGGATTAACGAGGAAAGACATGTGAGCA 3609  
Db 1719 AAGCGGTAATACGTTTATCCACGAATCAGGGGATTAACGAGGAAAGACATGTGAGCA 1778  
Qy 3610 AAAGGCCAGCAAAAGGCGCAGAACCGTAAAGCCCGCTTGTGCGGTTTTCATAGG 3669  
Db 1779 AAAGGCCAGCAAAAGGCGCAGAACCGTAAAGCCCGCTTGTGCGGTTTTCATAGG 1838  
Qy 3670 CTCGCGCCCTTCAAGCAGCATCAAAAATTCAGCGCTCAAGTTCAGAGGTGCGGAAACCCG 3729  
Db 1839 CTCGCGCCCTTCAAGCAGCATCAAAAATTCAGCGCTCAAGTTCAGAGGTGCGGAAACCCG 1898  
Qy 3730 ACAGGACTATAAAGATACAGGGCTTTCCCTCGGAAAGCTCCCTCGTGCCTCTCTCTGTT 3789  
Db 1899 ACAGGACTATAAAGATACAGGGCTTTCCCTCGGAAAGCTCCCTCGTGCCTCTCTCTGTT 1958  
Qy 3790 CCGACCTCGCGCTTACCGGATACCTGCTCCGCTTTCTCCCTTCGGGAAGCTCGCGCTT 3849  
Db 1959 CCGACCTCGCGCTTACCGGATACCTGCTCCGCTTTCTCCCTTCGGGAAGCTCGCGCTT 2018  
Qy 3850 TCTCATAGCTCACGCTGTAGGTATCTCAGTTTGGTGTAGGTCTGCTCGCTCAAGCTGGGC 3909  
Db 2019 TCTCATAGCTCACGCTGTAGGTATCTCAGTTTGGTGTAGGTCTGCTCGCTCAAGCTGGGC 2078  
Qy 3910 TGTGTGACGAAACCCCGCTTACGCCGACCGCTGCGCTTATCCGGTAACTATCTGCTT 3969  
Db 2079 TGTGTGACGAAACCCCGCTTACGCCGACCGCTGCGCTTATCCGGTAACTATCTGCTT 2138
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Qy	3970	GAGTCCACCCGGTAAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATT	4029
Db	2139		
		GAGTCCAAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATT	2198
Qy	4030	AGCAGACGCGAGTATGTAGGCGGTGCTACAGAGTCTTTGAAGTGGTGGCCTTAACCTACGGC	4089
Db	2199	AGCAGACGCGAGTATGTAGGCGGTGCTACAGAGTCTTTGAAGTGGTGGCCTTAACCTACGGC	2258
Qy	4090	TACACTAGAAGAACAGTATTTGGTATCTGGCTCTGTGAAGCAGATTACCTTCGGAAAA	4149
Db	2259	TACACTAGAAGAACAGTATTTGGTATCTGGCTCTGTGAAGCAGATTACCTTCGGAAAA	2318
Qy	4150	AGAGTTGGTAGCTCTTGATTCGGCAAAACAACACACCGCTGGTAGCGGTGGTTTTTGGTT	4209
Db	2319	AGAGTTGGTAGCTCTTGATTCGGCAAAACAACACACCGCTGGTAGCGGTGGTTTTTGGTT	2378
Qy	4210	TGCAAGCAGCAGATTATCGCGCAGAAAAAAGGATCTCAAGAAGATCTTTTGATCTTTTCT	4269
Db	2379	TGCAAGCAGCAGATTATCGCGCAGAAAAAAGGATCTCAAGAAGATCTTTTGATCTTTTCT	2438
Qy	4270	ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAAGGCGATAGAAGGCGATGCGCTGCGAA	4329
Db	2439	ACGGGGTCTGACGCTCAGAAGAACTCGTCAAGAAAGGCGATAGAAGGCGATGCGCTGCGAA	2498
Qy	4330	TCGGGAGCGGGATACCGTAAAGCACAGGAAGCGGTACGCCATTCGCGCCCAAGCTCT	4389
Db	2499	TCGGGAGCGGGATACCGTAAAGCACAGGAAGCGGTACGCCATTCGCGCCCAAGCTCT	2558
Qy	4390	TCAGCAATATCACGGGTAGCCAAACGCTATGTCTGTATAGCGGTCCGCCACACCCAGCCGG	4449
Db	2559	TCAGCAATATCACGGGTAGCCAAACGCTATGTCTGTATAGCGGTCCGCCACACCCAGCCGG	2618
Qy	4450	CCAAGTCGATGAATCCAGAAAAAGCGGCATTTTTCACCAATATTCGGCAAGCAGGCA	4509
Db	2619	CCAAGTCGATGAATCCAGAAAAAGCGGCATTTTTCACCAATATTCGGCAAGCAGGCA	2678
Qy	4510	TCGCCATGGGTACAGACGAGATCCTCGCGTCGGGCATGCGCCTTGAGCCTGGCGAAC	4569
Db	2679	TCGCCATGGGTACAGACGAGATCCTCGCGTCGGGCATGCGCCTTGAGCCTGGCGAAC	2738
Qy	4570	AGTTCCGCTGGCGGAGCCCTGATGTCTTCTGTCCAGATCATCTCTGATCGAACAGCCG	4629
Db	2739	AGTTCCGCTGGCGGAGCCCTGATGTCTTCTGTCCAGATCATCTCTGATCGAACAGCCG	2798
Qy	4630	GCTTCCATCCGAGTACGTGCTCGATGGATGTTTTCGGTTGGTGGTGGTGGGCGAG	4689
Db	2799	GCTTCCATCCGAGTACGTGCTCGATGGATGTTTTCGGTTGGTGGTGGTGGGCGAG	2858
Qy	4690	GTAGCCGATCAACGCTATGCAGCCGCGATGTCATCAGCCATGATGATCTTTCTCG	4749
Db	2859	GTAGCCGATCAACGCTATGCAGCCGCGATGTCATCAGCCATGATGATCTTTCTCG	2918
Qy	4750	GCAGGAGCAAGGTGAGATGACAGGAGATCCTTGCCCGGCACTTCGCCCATAAGCAGCCAG	4809
Db	2919	GCAGGAGCAAGGTGAGATGACAGGAGATCCTTGCCCGGCACTTCGCCCATAAGCAGCCAG	2978
Qy	4810	TCCCTTCGCGTTCAGTGACAAAGTCAGACACAGCTCGGCAAGAAAGCCCGCTGGGCC	4869
Db	2979	TCCCTTCGCGTTCAGTGACAAAGTCAGACACAGCTCGGCAAGAAAGCCCGCTGGGCC	3038
Qy	4870	AGCCACGATAGCCGCTGCTCGTCTGAGTTTCAATTCAGGCGCACCGACAGCTCGGTC	4929
Db	3039	AGCCACGATAGCCGCTGCTCGTCTGAGTTTCAATTCAGGCGCACCGACAGCTCGGTC	3098
Qy	4930	TTGACAAAAAGAAACCGGGCGCCCTCGCTGCTGACAGCGCGAACCGCGGCTCAGAGCAG	4989
Db	3099	TTGACAAAAAGAAACCGGGCGCCCTCGCTGCTGACAGCGCGAACCGCGGCTCAGAGCAG	3158
Qy	4990	CCGATTGTCTTTGTGCGCAGTCAATAGCGGAATAGCTCTTCACCCAAAGCGGCGCGAGAA	5049
Db	3159	CCGATTGTCTTTGTGCGCAGTCAATAGCGGAATAGCTCTTCACCCAAAGCGGCGCGAGAA	3218

Qy	5050	CCTGCGTGAACATCAATCTTGTTC	CAATCATGCGAAACGATCCTCATCTGTCCTTGTATCA	5109
Db	3219	CCTGCGTGAACATCAATCTTGTTC	CAATCATGCGAAACGATCCTCATCTGTCCTTGTATCA	3278
Qy	5110	GATCTTGATCCCTGGGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTG		5169
Db	3279	GATCTTGATCCCTGGGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTG		3338
Qy	5170	CAGGGCTTCCCAACCTTACACAGAGGGCGCCACAGCTGGGCAATTCGGTTTCGCTTGCCTGTC		5229
Db	3339	CAGGGCTTCCCAACCTTACACAGAGGGCGCCACAGCTGGGCAATTCGGTTTCGCTTGCCTGTC		3398
Qy	5230	CATAAACCCGCCAGCTAGCACTGTTGGGAAGGGCGATCGGTGCGGGCTCTTCGCTA		5289
Db	3399	CATAAACCCGCCAGCTAGCACTGTTGGGAAGGGCGATCGGTGCGGGCTCTTCGCTA		3458
Qy	5290	TTAGCCAGCTGCGAAAGGGGATGTGCTGCAAGCGGATTAAGTTGGGTAAACGCCAGGG		5349
Db	3459	TTAGCCAGCTGCGAAAGGGGATGTGCTGCAAGCGGATTAAGTTGGGTAAACGCCAGGG		3518
Qy	5350	TTTTCCAGTCACGAC	5365	
Db	3519	TTTTCCAGTCACGAC	3534	
RESULT 11				
US-10-395-709-12				
; Sequence 12, Application US/10395709				
; Publication No. US20040014645A1				
; GENERAL INFORMATION:				
; APPLICANT: ADVISYS				
; TITLE OF INVENTION: INCREASED DELIVERY OF A NUCLEIC ACID CONSTRUCT IN VIVO B1				
; TITLE OF INVENTION: GLUTAMATE ("PLG") SYSTEM				
; FILE REFERENCE: 108328.00115 - AVSI-0021P1				
; CURRENT APPLICATION NUMBER: US/10/395,709				
; CURRENT FILING DATE: 2003-03-24				
; NUMBER OF SEQ ID NOS: 25				
; SOFTWARE: PatentIn version 3.1				
; SEQ ID NO 12				
; LENGTH: 3534				
; TYPE: DNA				
; ORGANISM: artificial sequence				
; FEATURE:				
; OTHER INFORMATION: Sequence for the operatively linked components of the TI				
; OTHER INFORMATION: smid.				
US-10-395-709-12				
Query Match 39.8%; Score 2160; DB 7; Length 3534;				
Best Local Similarity 99.5%; Pred. No. 0;				
Matches 2166; Conservative 0; Mismatches 10; Indels 0; Gaps 0;				
Qy	3190	GAGCGAGGAAACAAGCTCAGCTTTTCTCCCTTTAGTGAGGGTTAATTTTCGAGCTTGGCG	3249	
Db	1359	GAGGGGGGGCCCCGATACCACTTTTGTCTTCTTTAGTGAGGGTTAATTTTCGAGCTTGGCG	1418	
Qy	3250	TAATCATGTGTCATAGCTGTTTCTCTGTGTGAATTTGTATCCCGCTCAAAATTCACACAAC	3309	
Db	1419	TAATCATGTGTCATAGCTGTTTCTCTGTGTGAATTTGTATCCCGCTCAAAATTCACACAAC	1478	
Qy	3310	ATACGAGCGGGAAGCATAAAGTGTAAAGCTTGGGGTGCCTAATAGTGAGCTAACTCACA	3369	
Db	1479	ATACGAGCGGGAAGCATAAAGTGTAAAGCTTGGGGTGCCTAATAGTGAGCTAACTCACA	1538	
Qy	3370	TTAATTTCCGTTGGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTGTCGCGAGCTGCAT	3429	
Db	1539	TTAATTTCCGTTGGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTGTCGCGAGCTGCAT	1598	
Qy	3430	TAATGAATCGGCCAAACGCGCGGGGAGAGCGGTTTCCGTATTTGGGGCGCTCTTCCGCTTCC	3489	
Db	1599	TAATGAATCGGCCAAACGCGCGGGGAGAGCGGTTTCCGTATTTGGGGCGCTCTTCCGCTTCC	1658	
Qy	3490	TCGCTCACTGACTCGCTCGGCTCGGTTCGCTCGGCTCGGCGAGCGGTATCAGCTCACTCA	3549	

; OTHER INFORMATION: smid. us-10-395-709-13									
Query Match 39.8%; Score 2160; DB 7; Length 3534; Best Local Similarity 99.5%; Pred. No. 0; Matches 2166; Conservative 0; Mismatches 10; Indels 0; Gaps 0;									
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Db	1359	GAGGGGGGGCCGGTACCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTTTCAGCTTGGCG	1418						
Qy	3250	TAATCATGCTCATAGCTTTTCCCTGCTGAATTTTATCGCTCACAATTTCCACACAAC	3309						
Db	1419	TAATCATGCTCATAGCTTTTCCCTGCTGAATTTTATCGCTCACAATTTCCACACAAC	1478						
Qy	3310	ATACGAGCCGGAACATAAAGTGTAAAGCTTGGGGTGCCTAAATCAGTGAGCTAACTCACA	3369						
Db	1479	ATACGAGCCGGAACATAAAGTGTAAAGCTTGGGGTGCCTAAATCAGTGAGCTAACTCACA	1538						
Qy	3370	TTAATTGCGTTGGCTCACTGCCCGCTTCCAGTCGGGAACCTGTCTGTCACAGCTGCAT	3429						
Db	1539	TTAATTGCGTTGGCTCACTGCCCGCTTCCAGTCGGGAACCTGTCTGTCACAGCTGCAT	1598						
Qy	3430	TAATGAATCGGCCNAACCGCGGGGAGAGCGGTTCGCTATTGGGCGCTCTTCGGCTTCC	3489						
Db	1599	TAATGAATCGGCCNAACCGCGGGGAGAGCGGTTCGCTATTGGGCGCTCTTCGGCTTCC	1658						
Qy	3490	TCGCTCACTGACTCGCTGCGCTCGCTGCTTCCAGTCCGGAGCGGTATCAGCTCACTCA	3549						
Db	1659	TCGCTCACTGACTCGCTGCGCTCGCTGCTTCCAGTCCGGAGCGGTATCAGCTCACTCA	1718						
Qy	3550	AAGCGGTAAATACGGTTATCCAGAAATCAGGGGATAACCGCAGGAAGAAATGTGAGCA	3609						
Db	1719	AAGCGGTAAATACGGTTATCCAGAAATCAGGGGATAACCGCAGGAAGAAATGTGAGCA	1778						
Qy	3610	AAAGGCCAGAAAAGGCCAGAACCGTAAAGGCCGCTGTGCTGGGTTTTCATAGG	3669						
Db	1779	AAAGGCCAGAAAAGGCCAGAACCGTAAAGGCCGCTGTGCTGGGTTTTCATAGG	1838						
Qy	3670	CTCGCCCTCTGACGAGCATCAAAAATTCAGAGCTCAAGTCAGAGGTGCGGAACCCG	3729						
Db	1839	CTCGCCCTCTGACGAGCATCAAAAATTCAGAGCTCAAGTCAGAGGTGCGGAACCCG	1898						
Qy	3730	ACAGGACTATAAAGATACCAAGGGTTTCCCTCTGGAAGCTCCCTCGTGCCTCTCTCTGT	3789						
Db	1899	ACAGGACTATAAAGATACCAAGGGTTTCCCTCTGGAAGCTCCCTCGTGCCTCTCTCTGT	1958						
Qy	3790	CCGACCTCGCGCTTACCGGATACCTGTGCGCTTTCTCCCTTCGGGAAGCGTGGCGCTT	3849						
Db	1959	CCGACCTCGCGCTTACCGGATACCTGTGCGCTTTCTCCCTTCGGGAAGCGTGGCGCTT	2018						
Qy	3850	TCTCATAGCTCAGCTGTAGTATCTCAGTTCGGTGTAGTGTCTGCTCAAGCTGGGC	2078						
Db	2019	TCTCATAGCTCAGCTGTAGTATCTCAGTTCGGTGTAGTGTCTGCTCAAGCTGGGC	2138						
Qy	3910	TGTGTGCAAGAACCCCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATCGCTTT	3969						
Db	2079	TGTGTGCAAGAACCCCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATCGCTTT	2138						
Qy	3970	GAGTCCAAACCGGTAAAGACAGCTTATTCGGCATCTGGCAGCAGCACTGGTAACAGATT	4029						
Db	2139	GAGTCCAAACCGGTAAAGACAGCTTATTCGGCATCTGGCAGCAGCACTGGTAACAGATT	2198						
Qy	4030	AGCAGAGCAGGTATGTAGGCGGTGTACAGAGTTCTTGAAGTGTGGCTTAACACTAGGC	4089						
Db	2199	AGCAGAGCAGGTATGTAGGCGGTGTACAGAGTTCTTGAAGTGTGGCTTAACACTAGGC	2258						
Qy	4090	TACATAGAAAGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACTCTTCGGA	4149						
Db	2259	TACATAGAAAGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACTCTTCGGA	2318						
Qy	4150	AGAGTTGGTAGCTTCTGATCCGGCAACAAACCAACCGCTGGTACGGTGGTTTTTTGTT	4209						
Db									

Db	2319	AGAGTTGGTAGCTTCTGATCCGGCAACAAACCAACCGCTGGTACGGTGGTTTTTTGTT	2378						
Qy	4210	TGCAAGCAGCAGATTACCGCGCAGAAAAAAGGATCTCAAGAAAGATCTTTGATCTTTCT	4269						
Db	2379	TGCAAGCAGCAGATTACCGCGCAGAAAAAAGGATCTCAAGAAAGATCTTTGATCTTTCT	2438						
Qy	4270	ACGGGTCTGACGCTCAGAAAGAACTCTGTCAAGAGGCGATAGAAAGGCGATCGCTCGAA	4329						
Db	2439	ACGGGTCTGACGCTCAGAAAGAACTCTGTCAAGAGGCGATAGAAAGGCGATCGCTCGAA	2498						
Qy	4330	TCGGGAGCGCGATACCGTAAACACGAGGAAGGGTTCAGCCCATTCGCCGCCAAGCTCT	4389						
Db	2499	TCGGGAGCGCGATACCGTAAACACGAGGAAGGGTTCAGCCCATTCGCCGCCAAGCTCT	2558						
Qy	4390	TCAGCAATATCAGCGGTAGCCAAACGCTATCTCTGTAGCGGTCCGCGCACACCCAGCGCG	4449						
Db	2559	TCAGCAATATCAGCGGTAGCCAAACGCTATCTCTGTAGCGGTCCGCGCACACCCAGCGCG	2618						
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Qy	4510	TCGCCATGGGTACGACGAGATCTCGCGTCCGGGATCGCGCTTGAGCCTGGCGAAC	4569						
Db	2679	TCGCCATGGGTACGACGAGATCTCGCGTCCGGGATCGCGCTTGAGCCTGGCGAAC	2738						
Qy	4570	AGTTCCGCTGGCGGAGCCCTGATGCTCTTCGTCCAGATCATCTGATCGACAAGACCG	4629						
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Qy	4630	GCTTCCATCCGAGTACGCTGCTCGATGCGATGTTTTCCGTTGGTGGTGAATGGGCGAG	4689						
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Qy	4690	GTAGCCGATCAGCGCTGATGACGCGCCGATTCGATCGAGATCATCGCATGATCTTCTCG	4749						
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Qy	4750	GCAGGAGCAAGGTGAGATGACAGGAGATCTTCGCCCGGCACTTCGCCCAATAGCAGCGAG	4809						
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Qy	4930	TTGACAAAAGAAACCGGGGCGCCCTCGCTGACAGCGGAAACACGGCGGATCAGAGCAG	4989						
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Qy	4990	CCGATTGTCTGTTGCCAGTCAATAGCCGAATAGCTTCCACCAAGCGCGGAGAA	5049						
Db	3159	CCGATTGTCTGTTGCCAGTCAATAGCCGAATAGCTTCCACCAAGCGCGGAGAA	3218						
Qy	5050	CTGCGCTGCATTCATCTTTGTTCAATCATGCGAAACGATCCTCATCTGTCTCTTGATCA	5109						
Db	3219	CTGCGCTGCATTCATCTTTGTTCAATCATGCGAAACGATCCTCATCTGTCTCTTGATCA	3278						
Qy	5110	GATCTTTGATCCCTCGCCCATCAGATCTTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG	5169						
Db	3279	GATCTTTGATCCCTCGCCCATCAGATCTTTGGCGGCAAGAAAGCCATCCAGTTTACTTTG	3338						
Qy	5170	CAGGGCTTCCCAACCTTACAGAGGCGCCCGCAGCTGGCAATTCGCGTTCCGTTGCTGTC	5229						
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Qy	5230	CATAAAACCGCCAGCTAGCACTGTTGGGAAGGGGATCGGTCGGGCGCTCTTCGCTA	5289						
Db	3399	CATAAAACCGCCAGCTAGCACTGTTGGGAAGGGGATCGGTCGGGCGCTCTTCGCTA	3458						


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QY 5050 CTGCGGTGCAATCCATCTTGTTCATCATCGAAACGATCCTCATCTGTCTCTTGATCA 5109
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QY 5110 GATCTTGATCCCTGCGCCATCAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTGG 5169
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RESULT 14

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US-10-395-709-15
; Sequence 15, Application US/10395709
; Publication No. US20040014645A1
; GENERAL INFORMATION:
; APPLICANT: Advivis
; TITLE OF INVENTION: INCREASED DELIVERY OF A NUCLEIC ACID CONSTRUCT IN VIVO BY THE POL
; FILE REFERENCE: 108328.00115 - AVSI-0021P1
; CURRENT APPLICATION NUMBER: US/10/395,709
; CURRENT FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is the entire plasmid sequence for wildtype GHRH.
US-10-395-709-15
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Best Local Similarity 99.5%; Pred. No. 0;
Matches 2166; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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QY 3490 TCGCTCACTGACTCGCTGCGCTCGGTCGTTGCGCTGCGGCGAGCGGTATCAGCTCACTCA 3549
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QY 3550 AAGGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGACGAAAGAACATGTGAGCA 3609
Db 1719 AAGGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGACGAAAGAACATGTGAGCA 1778
QY 3610 AAGGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGACGAAAGAACATGTGAGCA 3669
Db 1779 AAGGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGACGAAAGAACATGTGAGCA 1838
QY 3670 CTCGCGCCCTCGAAGAGATACCAAGAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 3729
Db 1839 CTCGCGCCCTCGAAGAGATACCAAGAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG 1898
QY 3730 ACAGGACTATAAGATACCAAGGTTTCCCTGGAAGCTCCCTGCGGCTCTCTCTGTT 3789
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[illegible]

RESULT 15

RESULTS IS
US-10-359-919A-11

US-10-339-919A-II
: Sequence 11. Application US/10359919A

; sequence II, APPLICATION US/103
: Publication No. US20040038978A1

Publication No: US20070103600A1

APPLICANT: Baylor College of Medicine

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OM nucleic - nucleic search, using sw model

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Title: US-10-798-896-1

Perfect score: 5423

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Gapop 10.0 , Gapext 1.0

Searched: 7204323 seqs, 1061406715 residues

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Listing first 45 summaries

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 - 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2160	39.8	3534	12	US-11-186-282-22
2	1773	32.7	2722	12	Sequence 22, Appl
3	1773	32.7	2725	12	Sequence 23, Appl
4	1771.4	32.7	2700	12	Sequence 24, Appl
5	1771.4	32.7	2716	12	Sequence 33, Appl
6	1771.4	32.7	2716	12	Sequence 27, Appl
7	1771.4	32.7	2716	12	Sequence 28, Appl
8	1771.4	32.7	2716	12	Sequence 29, Appl
9	1771.4	32.7	2721	12	Sequence 31, Appl
10	1771.4	32.7	2721	12	Sequence 26, Appl
11	1771.4	32.7	2725	12	Sequence 34, Appl
12	1771.4	32.7	2725	12	Sequence 25, Appl
13	1771.4	32.7	2739	12	Sequence 30, Appl
14	1771.4	32.7	2739	12	Sequence 32, Appl
15	1372.8	25.3	2403	7	US-10-523-682-1
16	1347.2	24.8	5181	12	Sequence 1, Appl
17	1347.2	24.8	5181	12	Sequence 3, Appl
18	1082.6	20.0	4968	12	Sequence 19, Appl
19	1082.6	20.0	5073	12	Sequence 18, Appl
20	1082.2	20.0	8953	12	Sequence 8, Appl
21	1082.2	20.0	8953	12	Sequence 64, Appl

c 21	1081.2	19.9	5094	12	US-11-024-251-28	Sequence 28, Appl
c 22	1081.2	19.9	5103	12	US-11-024-251-26	Sequence 26, Appl
c 23	1081.2	19.9	5766	12	US-11-024-251-34	Sequence 34, Appl
c 24	1081.2	19.9	5972	12	US-11-024-251-30	Sequence 30, Appl
c 25	1081.2	19.9	6197	12	US-11-024-251-32	Sequence 32, Appl
c 26	1080.6	19.9	11110	7	US-10-978-927-20	Sequence 20, Appl
c 27	1080.6	19.9	12263	7	US-10-978-927-19	Sequence 19, Appl
c 28	1080	19.9	3448	12	US-11-024-959-773	Sequence 773, Appl
c 29	1080	19.9	5534	12	US-11-024-959-776	Sequence 776, Appl
c 30	1080	19.9	7160	12	US-11-024-959-777	Sequence 777, Appl
c 31	1079.4	19.9	5001	12	US-11-214-613-40	Sequence 40, Appl
c 32	1079.4	19.9	5034	12	US-11-214-613-33	Sequence 33, Appl
c 33	1079.4	19.9	5164	12	US-11-214-613-36	Sequence 36, Appl
c 34	1079.4	19.9	5277	12	US-11-214-613-25	Sequence 25, Appl
c 35	1079.4	19.9	5295	12	US-11-214-613-38	Sequence 38, Appl
c 36	1079.4	19.9	5327	12	US-11-214-613-27	Sequence 27, Appl
c 37	1079.4	19.9	5337	12	US-11-214-613-19	Sequence 19, Appl
c 38	1079.4	19.9	5337	12	US-11-214-613-23	Sequence 23, Appl
c 39	1079.4	19.9	5337	12	US-11-214-613-31	Sequence 31, Appl
c 40	1079.4	19.9	5338	12	US-11-214-613-15	Sequence 15, Appl
c 41	1079.4	19.9	5338	12	US-11-214-613-29	Sequence 29, Appl
c 42	1079.4	19.9	5345	12	US-11-214-613-17	Sequence 17, Appl
c 43	1079.4	19.9	5387	12	US-11-214-613-41	Sequence 41, Appl
c 44	1079.4	19.9	5395	12	US-11-214-613-21	Sequence 21, Appl
c 45	1079.4	19.9	7239	12	US-11-089-551A-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-11-186-282-22
; Sequence 22, Application US/11/186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: Advicys, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 22
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Plasmid vector having an analog GHRH sequence.
US-11-186-282-22

Query Match	39.8%	Score 2160;	DB 12;	Length 3534;
Best Local Similarity	99.5%	Pred. No. 0;		
Matches 2166;	Conservative	0;	Mismatches 10;	Indels 0; Gaps 0;
QY	3190	GAGCCAGGGAACAAGCTCAGCTTTTGTTCCTTTAGTGAGGGTTAATTTCCAGCTTGCGG	3249	
Db	1359	GAGGGGGGCCCGGTACACAGCTTTTGTTCCTTTAGTGAGGGTTAATTTCCAGCTTGCGG	1418	
QY	3250	TAATCATGTCATAGCTGTTTCTGTGTGAATTTATCCGCTCACAATTCACACAAC	3309	
Db	1419	TAATCATGTCATAGCTGTTTCTGTGTGAATTTATCCGCTCACAATTCACACAAC	1478	
QY	3310	ATACGAGCGGGAAGCATAAAGTGAAGCTGGGGTCCCTTAATGAGTGAGCTAACTCACA	3369	
Db	1479	ATACGAGCGGGAAGCATAAAGTGAAGCTGGGGTCCCTTAATGAGTGAGCTAACTCACA	1538	
QY	3370	TTAATTTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTCAGCTGCAT	3429	
Db	1539	TTAATTTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTCAGCTGCAT	1598	
QY	3430	TAATGAATCGGCCAACCGCGGGGAGAGCGGTTTCGGTATTGGGCGCTCTTCGGCTTCC	3489	
Db	1599	TAATGAATCGGCCAACCGCGGGGAGAGCGGTTTCGGTATTGGGCGCTCTTCGGCTTCC	1658	

; FEATURE:									
; OTHER INFORMATION: Plasmid vector having a codon optimized mouse GHRH sequence									
US-11-186-282-23									
Query Match 32.78; Score 1773; DB 12; Length 2722;									
Best Local Similarity 98.6%; Pred. No. 0;									
Matches 1803; Conservative 0; Mismatches 15; Indels 11; Gaps 1;									
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DB	860	AGTGAGGTTAAATTCAGACTTGGTCTTCCGCTTCTCGCTCACTGACTCGCTCGCGCTCG	919						
QY	3514	GTGCTTCGCTGCGCGAGCGGTATCAGCTCACTCAAGGCGGTATACCGGTTATCCACA	3573						
DB	920	GTGCTTCGCTGCGCGAGCGGTATCAGCTCACTCAAGGCGGTATACCGGTTATCCACA	979						
QY	3574	GAATCAGGGGATACCGAGCAAGAACATCTGAGCAAAAGGCCAGAAAGGCCAGGAAC	3633						
DB	980	GAATCAGGGGATACCGAGCAAGAACATCTGAGCAAAAGGCCAGAAAGGCCAGGAAC	1039						
QY	3634	CGTAAAGGCGCGTTCGCTGCGGCTTTTCCATAGGCTCCGCCCTCGAGCATCAC	3693						
DB	1040	CGTAAAGGCGCGTTCGCTGCGGCTTTTCCATAGGCTCCGCCCTCGAGCATCAC	1099						
QY	3694	AAAAATCGACGCTCAAGTCAAGGTGCGGAAACCCGACAGGACTATATAAGATACAGGCG	3753						
DB	1100	AAAAATCGACGCTCAAGTCAAGGTGCGGAAACCCGACAGGACTATATAAGATACAGGCG	1159						
QY	3754	TTTCCCGCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCCTGCGCTTACCGGATAC	3813						
DB	1160	TTTCCCGCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCCTGCGCTTACCGGATAC	1219						
QY	3814	CTGTCCGCTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTAT	3873						
DB	1220	CTGTCCGCTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTAT	1279						
QY	3874	CTCAGTTCGCTGAGTTCGCTCCAAAGTGGCTGTGTGCAAGAACCCCGCTTCAG	3933						
DB	1280	CTCAGTTCGCTGAGTTCGCTCCAAAGTGGCTGTGTGCAAGAACCCCGCTTCAG	1339						
QY	3934	CCGACCGCTCGGCTTATCCGCTTACTATCTGTTGAGTCCAAACCGGTAAAGACGAC	3993						
DB	1340	CCGACCGCTCGGCTTATCCGCTTACTATCTGTTGAGTCCAAACCGGTAAAGACGAC	1399						
QY	3994	TTATCGCCTACGTCAGCAGCCTTGGTAAACAGGATAGCAGAGCGAGTATGTAGCGGT	4053						
DB	1400	TTATCGCCTACGTCAGCAGCCTTGGTAAACAGGATAGCAGAGCGAGTATGTAGCGGT	1459						
QY	4054	GCTACAGAGTTCCTGAAGTGGTGGCTTAACCTACGCTTACACTAGAAGAACAGTATTGGT	4113						
DB	1460	GCTACAGAGTTCCTGAAGTGGTGGCTTAACCTACGCTTACACTAGAAGAACAGTATTGGT	1519						
QY	4114	ATCTGCGCTCTGTAAGCCAGTTACCTTCGGAAGAGTTCGTAAGTTCCTGATCCGCG	4173						
DB	1520	ATCTGCGCTCTGTAAGCCAGTTACCTTCGGAAGAGTTCGTAAGTTCCTGATCCGCG	1579						
QY	4174	AAACAAACCAACCGCTGGTAGCGGTGTTTTTTTGTGTTGCAAGCAGCAGATTTAGCGCAGA	4233						
DB	1580	AAACAAACCAACCGCTGGTAGCGGTGTTTTTTTGTGTTGCAAGCAGCAGATTTAGCGCAGA	1639						
QY	4234	AAAAAGGATCTCAAGAGATCTCTTGTATCTTTTCTACGGGCTCTGA-----CG	4282						
DB	1640	AAAAAGGATCTCAAGAGATCTCTTGTATCTTTTCTACGGGCTCTGAAGCTCAGTAGCG	1699						
QY	4283	CTCAGAAGACTGCTCAAGAGGCGGATAGAGGCGATGCGCTCGGAATCGGGAGCGCGGA	4342						
DB	1700	CTCAGAAGACTGCTCAAGAGGCGGATAGAGGCGATGCGCTCGGAATCGGGAGCGCGGA	1759						
QY	4343	TACGTTAAACACGAGCAAGCGGTTCAGCCATTCGCGCCCAAGCTCTTCAGCAATATCAC	4402						
DB	1760	TACGTTAAACACGAGCAAGCGGTTCAGCCATTCGCGCCCAAGCTCTTCAGCAATATCAC	1819						
QY	4403	GGGTAGCCAAACGCTATGTCTCTGATAGCGGTCCGCCACACCCAGCCGCGCCACAGTCGATGA	4462						

RESULT 3
US-11-186-282-24
; Sequence 24, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: Advisys, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24

DB	1820	GGGTAGCCAAACGCTATGTCTGTATAGCGGTCCGCCACACCCAGCCGCGCCACAGTCGATGA	1879						
QY	4463	ATCCAGAAAGCGGCCATTTTCCACCATGATATTTCCGCAAGCAGGAGGATCCGCCATGGGTCA	4522						
DB	1880	ATCCAGAAAGCGGCCATTTTCCACCATGATATTTCCGCAAGCAGGAGGATCCGCCATGGGTCA	1939						
QY	4523	CGACGAGATCTCTCGCGCTCGGCGATCGCGCTTTGAGCCCTGGCGAAACAGTTCGGCTGGCG	4582						
DB	1940	CGACGAGATCTCTCGCGCTCGGCGATCGCGCTTTGAGCCCTGGCGAAACAGTTCGGCTGGCG	1999						
QY	4583	CGAGCCCTGATGCTCTTCTGTCAGATCATCTCTGATCGCAAGACCGGCTTCCATCCGAG	4642						
DB	2000	CGAGCCCTGATGCTCTTCTGTCAGATCATCTCTGATCGCAAGACCGGCTTCCATCCGAG	2059						
QY	4643	TACGTCTCTGCTCGATCGATGTTTCGCTTGGTGGTTCGAATGGGAGGAGTAGCCGGATCAA	4702						
DB	2060	TACGTCTCTGCTCGATCGATGTTTCGCTTGGTGGTTCGAATGGGAGGAGTAGCCGGATCAA	2119						
QY	4703	GGGTATGCAAGCCCGCATTTGCAATAGCCATGATGATATCTTCTCGGCAGGACAAAGGT	4762						
DB	2120	GGGTATGCAAGCCCGCATTTGCAATAGCCATGATGATATCTTCTCGGCAGGACAAAGGT	2179						
QY	4763	GAGATGACAGGAGATCTTCCCGCGGCACTTCCGCCAATAGCAGCCAGTCCCTTCCCGCTT	4822						
DB	2180	GAGATGACAGGAGATCTTCCCGCGGCACTTCCGCCAATAGCAGCCAGTCCCTTCCCGCTT	2239						
QY	4823	CAGTGACAAAGCTGACGACACAGCTTGCACAAAGGAACCGCGTGGCCAGCAGCATAGACC	4882						
DB	2240	CAGTGACAAAGCTGACGACACAGCTTGCACAAAGGAACCGCGTGGCCAGCAGCATAGACC	2299						
QY	4883	GGCTGCTCTGCTCTGCTGAGTTCAATTCAGGGCACCGGACAGGTCGCTTTGACAAAAAGAA	4942						
DB	2300	GGCTGCTCTGCTCTGCTGAGTTCAATTCAGGGCACCGGACAGGTCGCTTTGACAAAAAGAA	2359						
QY	4943	CGGGCGCCCTGCTGCTGAGCAGCGGAAACACCGCGGCAATCAGAGCAGCCGATGTCGTT	5002						
DB	2360	CGGGCGCCCTGCTGCTGAGCAGCGGAAACACCGCGGCAATCAGAGCAGCCGATGTCGTT	2419						
QY	5003	GTGCCAGTCAATGACCGCAATAGCTCTCCACCAAGCGCGGAGAACCTGCGTGCAATC	5062						
DB	2420	GTGCCAGTCAATGACCGCAATAGCTCTCCACCAAGCGCGGAGAACCTGCGTGCAATC	2479						
QY	5063	CATCTTGTTCATATCATGCAAAAGCTCTCATCTCTCTCTTGTATCAGATCTTGTATCCCC	5122						
DB	2480	CATCTTGTTCATATCATGCAAAAGCTCTCATCTCTCTCTTGTATCAGATCTTGTATCCCC	2539						
QY	5123	TGGCCATCAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGAGGGCTTCCCAA	5182						
DB	2540	TGGCCATCAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGAGGGCTTCCCAA	2599						
QY	5183	CTTTACAGAGGGCGCCCGCAGCTGGCAATTCGCTTGGTTCGTTCCATATAAACCGCCC	5242						
DB	2600	CTTTACAGAGGGCGCCCGCAGCTGGCAATTCGCTTGGTTCGTTCCATATAAACCGCCC	2659						
QY	5243	AGTCTAGCAACTGTTGGGAAGGCGGATCG	5271						
DB	2660	AGTCTAGCAACTGTTGGGAAGGCGGATCG	2688						

; LENGTH: 2725			
; TYPE: DNA			
; ORGANISM: artificial sequence			
; FEATURE:			
; OTHER INFORMATION: Plasmid vector having a codon optimized rat GHRH sequence			
US-11-186-282-24			
Query Match 32.78; Score 1773; DB 12; Length 2725;			
Best Local Similarity 98.68; Pred. No. 0;			
Matches 1803; Conservative 0; Mismatches 15; Indels 11; Gaps 1;			
Qy	3454	AGAGCGGCTTGGCGATTTGGCGCTCTTCGGCTTCCTCGCTCACTGACTCGCTCGCGCTCG	3513
Db	863	AGTGAGGGTTAAATTCGAGCTTGGCTTCCTCGCTCTCACTGACTCGCTCGCGCTCG	922
Qy	3514	GTCTTTTCGGCTGCGCGAGCGGTATACAGCTCACTCAAAGGGGTTATACGGTTATCCACA	3573
Db	923	GTCTTTTCGGCTGCGCGAGCGGTATACAGCTCACTCAAAGGGGTTATACGGTTATCCACA	982
Qy	3574	GAATCAGGGGTAACCGAGGAAAGAACATGTGACAAAGGCGCAGCAAAAGGCGCAGAAC	3633
Db	983	GAATCAGGGGTAACCGAGGAAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCGCAGAAC	1042
Qy	3634	CGTAAAAAGGCGCGTTGCTGGCGCTTTTTCATAGGCTCCGCCCTCGACGAGCATCAC	3693
Db	1043	CGTAAAAAGGCGCGTTGCTGGCGCTTTTTCATAGGCTCCGCCCTCGACGAGCATCAC	1102
Qy	3694	AAAAATCGAGCTCAAGTCAGAGGTGGCGAAACCCGACAGACTATAAAGATACAGGCG	3753
Db	1103	AAAAATCGAGCTCAAGTCAGAGGTGGCGAAACCCGACAGACTATAAAGATACAGGCG	1162
Qy	3754	TTTTCCCTCGAGCTCCCTCGTGGCTCTCTGTTCCGACCCCTGCGCTTACCGGATAC	3813
Db	1163	TTTTCCCTCGAGCTCCCTCGTGGCTCTCTGTTCCGACCCCTGCGCTTACCGGATAC	1222
Qy	3814	CTGTCGCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCAAGCTGTAGGTAT	3873
Db	1223	CTGTCGCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCAAGCTGTAGGTAT	1282
Qy	3874	CTCAGTTCCGCTGTAGGTGCTTGGCTCCAAAGTGGGCTGTGTGCACGAACCCCGCTTCAG	3933
Db	1283	CTCAGTTCCGCTGTAGGTGCTTGGCTCCAAAGTGGGCTGTGTGCACGAACCCCGCTTCAG	1342
Qy	3934	CCGACCGCTGCGCTTATCGGTAACTATCGTCTGAGTCCACCCGCTTAAGACACGAC	3993
Db	1343	CCGACCGCTGCGCTTATCGGTAACTATCGTCTGAGTCCACCCGCTTAAGACACGAC	1402
Qy	3994	TTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTAAGCAGCGAGGTATGTAGGCGGT	4053
Db	1403	TTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTAAGCAGCGAGGTATGTAGGCGGT	1462
Qy	4054	GCTACAGAGTTCTTGAAGTGGTGGCTTAACTACGGCTACACTAGAGAAACAGTATTTGGT	4113
Db	1463	GCTACAGAGTTCTTGAAGTGGTGGCTTAACTACGGCTACACTAGAGAAACAGTATTTGGT	1522
Qy	4114	ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGAGTTGCTAGCTCTTGATCCGCC	4173
Db	1523	ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGAGTTGCTAGCTCTTGATCCGCC	1582
Qy	4174	AAACAAACCCACCGCTGGTAGCGGTGGTTTTTTTGTGTGCAAGCAGCAGATTTACCGCAGA	4233
Db	1583	AAACAAACCCACCGCTGGTAGCGGTGGTTTTTTTGTGTGCAAGCAGCAGATTTACCGCAGA	1642
Qy	4234	AAAAAAGGATCTCAAGAGATCTTTTGATCTTTTCTACGGGCTCTGA-----CG	4282
Db	1643	AAAAAAGGATCTCAAGAGATCTTTTGATCTTTTCTACGGGCTCTGAAGCTAGCGTAGCG	1702
Qy	4283	CTCAGAGAGCTCTCAGAGGCGATAGAGGCGATCGCTGCGAATCGGAGCGCGGA	4342
Db	1703	CTCAGAGAGCTCTCAGAGGCGATAGAGGCGATCGCTGCGAATCGGAGCGCGGA	1762
Qy	4343	TACCGTAAAGCACGAGGAAGCGGTACGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAC	4402
Db			
Db	1763	TACCGTAAAGCACGAGGAAGCGGTACGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAC	1822
Qy	4403	GGGTAGCCCAACGCTATGTCTGATAGCGGTTCGCCCAACACCCAGCGGCCACAGTCCGATGA	4462
Db	1823	GGGTAGCCCAACGCTATGTCTGATAGCGGTTCGCCCAACACCCAGCGGCCACAGTCCGATGA	1882
Qy	4463	ATCCAGAAAGCGGCCATTTTTCACCATGATATTTCGGCAAGCAGGATCCGCTATGGGTCA	4522
Db	1883	ATCCAGAAAGCGGCCATTTTTCACCATGATATTTCGGCAAGCAGGATCCGCTATGGGTCA	1942
Qy	4523	CGACGAGATCCTCGCGTGGGCGATGCGCGCTTGAGCCTTGGCGAAACAGTTCGGCTGGCG	4582
Db	1943	CGACGAGATCCTCGCGTGGGCGATGCGCGCTTGAGCCTTGGCGAAACAGTTCGGCTGGCG	2002
Qy	4583	CGAGCCCTGATGCTCTTGTCCAGATCATCTCTGATCGCAACACCGGCTTCCATCCGAG	4642
Db	2003	CGAGCCCTGATGCTCTTGTCCAGATCATCTCTGATCGCAACACCGGCTTCCATCCGAG	2062
Qy	4643	TACGTGCTCGCTCGATGCGATGTTTTCGCTTGGTGGTTCGAATGGCGAGGTAGCCGGATCAA	4702
Db	2063	TACGTGCTCGCTCGATGCGATGTTTTCGCTTGGTGGTTCGAATGGCGAGGTAGCCGGATCAA	2122
Qy	4703	GCCTATGACAGCCCGCATTTGATCAGCCATGATGATATCTTCTCGGACGAGCAAGGT	4762
Db	2123	GCCTATGACAGCCCGCATTTGATCAGCCATGATGATATCTTCTCGGACGAGCAAGGT	2182
Qy	4763	GAGATGACAGGAGATCCTGCGCCCGGCACCTTCGCCCAATAGCAGCGAGTCCCTTCCGCTT	4822
Db	2183	GAGATGACAGGAGATCCTGCGCCCGGCACCTTCGCCCAATAGCAGCGAGTCCCTTCCGCTT	2242
Qy	4823	CAGTGAACAAGCTCGACGACAGCTGCGCAAGGAACCGCGCTGCGGACGACGATAGCC	4882
Db	2243	CAGTGAACAAGCTCGACGACAGCTGCGCAAGGAACCGCGCTGCGGACGACGATAGCC	2302
Qy	4883	GCCTGCTGCTCCTCGTTCAGTTCATTTCAGGACACCGGACAGGTCCGCTTTCGACAAAAGAA	4942
Db	2303	GCCTGCTGCTCCTCGTTCAGTTCATTTCAGGACACCGGACAGGTCCGCTTTCGACAAAAGAA	2362
Qy	4943	CCGGGCGCCCTGCGTGCACGCGGACACGCGGCGCATCAGACGAGCGGATGCTCTGTT	5002
Db	2363	CCGGGCGCCCTGCGTGCACGCGGACACGCGGCGCATCAGACGAGCGGATGCTCTGTT	2422
Qy	5003	GTGCCAGATCATAGCGCAATAGCTCTCCACCAAGCGCGCGGAGAACCTTCGCTGCAATC	5062
Db	2423	GTGCCAGATCATAGCGCAATAGCTCTCCACCAAGCGCGCGGAGAACCTTCGCTGCAATC	2482
Qy	5063	CATCTTTGTTCAATCATCGCAACGATCCTCATCTGTCTTGTATCAGATCTTGTATCCCC	5122
Db	2483	CATCTTTGTTCAATCATCGCAACGATCCTCATCTGTCTTGTATCAGATCTTGTATCCCC	2542
Qy	5123	TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTCAGGGGTTCCCAA	5182
Db	2543	TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTCAGGGGTTCCCAA	2602
Qy	5183	CTTTACAGAGGCGCGCCAGCTGGCAATTCGCGTTCGCTTGTCTCATATAAAACCGCCC	5242
Db	2603	CTTTACAGAGGCGCGCCAGCTGGCAATTCGCGTTCGCTTGTCTCATATAAAACCGCCC	2662
Qy	5243	AGTCTAGCAACTGTTGGGAAGGCGGATCG	5271
Db	2663	AGTCTAGCAACTGTTGGGAAGGCGGATCG	2691
RESULT 4			
US-11-186-282-33			
; Sequence 33, Application US/11186282			
; Publication No. US20060025368A1			
; GENERAL INFORMATION:			
; APPLICANT: Advisys, Inc.			
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response			
; FILE REFERENCE: 108328.000265 AVS1-0042			
; CURRENT APPLICATION NUMBER: US/11/186,282			
; CURRENT FILING DATE: 2005-07-21			

; NUMBER OF SEQ ID NOS: 41									
; SOFTWARE: PatentIn version 3.3									
; SEQ ID NO 33									
; LENGTH: 2700									
; TYPE: DNA									
; ORGANISM: artificial sequence									
; FEATURE:									
; OTHER INFORMATION: This is the optimized plasmid for Horse GHRH.									
US-11-186-282-33									
Query Match 32.7%; Score 1771.4; DB 12; Length 2700;									
Best Local Similarity 98.5%; Pred. No. 0;									
Matches 1802; Conservative 0; Mismatches 16; Indels 11; Gaps 1;									
QY	3454	AGAGCGGTTTGGCGTATTGGCGCTCTTCGCGCTCTTCGCTCACTGACTCGCTCGCGCTCG	3513						
DB	859	AGTGAGGTTAAATTTTCGAGCTTGGTCTTTCGCTTTCGCTCACTGACTCGCTCGCGCTCG	918						
QY	3514	GTGTTTCGGCTGGCGGAGCGGTATCAGCTCACTCAAGCGGTATACGGTTATCCACA	3573						
DB	919	GTGTTTCGGCTGGCGGAGCGGTATCAGCTCACTCAAGCGGTAAATACGGTTATCCACA	978						
QY	3574	GAATCAGGGATACCGCAGGAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC	3633						
DB	979	GAATCAGGGATACCGCAGGAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC	1038						
QY	3634	CGTAAAGGCCGCTTTCGCTGCTGCTGCTTTTCCATAGGCTCCGCCCTCGACGAGCATCAC	3693						
DB	1039	CGTAAAGGCCGCTTTCGCTGCTGCTGCTTTTCCATAGGCTCCGCCCTCGACGAGCATCAC	1098						
QY	3694	AAAAATCGACGCTCAAGTCAAGGTGGCGAAACCCGACAGGACTATAAGATACAGGGCG	3753						
DB	1099	AAAAATCGACGCTCAAGTCAAGGTGGCGAAACCCGACAGGACTATAAGATACAGGGCG	1158						
QY	3754	TTTCCCTCGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTCGCGCTTACCGGATAC	3813						
DB	1159	TTTCCCTCGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTCGCGCTTACCGGATAC	1218						
QY	3814	CTGTCCGCTTTCCTCCCTCGGGAAGGTGGCGCTTCTCATAGCTCACGCTGTAGGTAT	3873						
DB	1219	CTGTCCGCTTTCCTCCCTCGGGAAGGTGGCGCTTCTCATAGCTCACGCTGTAGGTAT	1278						
QY	3874	CTCAGTTTCGTTGAGTTCGCTCCAAAGTGGCTGTGTGCAAGAACCCCGCTTCAG	3933						
DB	1279	CTCAGTTTCGTTGAGTTCGCTCCAAAGTGGCTGTGTGCAAGAACCCCGCTTCAG	1338						
QY	3934	CCGACCGCTGGCGCTTATCCGTTAACTATCGTCTTGAGTCCAAACCGGTAAGACAGAC	3993						
DB	1339	CCGACCGCTGGCGCTTATCCGTTAACTATCGTCTTGAGTCCAAACCGGTAAGACAGAC	1398						
QY	3994	TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGT	4053						
DB	1399	TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGT	1458						
QY	4054	GCTACAGAGTTCTTGAAGTGGTGGCTTAACCTACGGCTACACTAGAAGAACAGTATTGGT	4113						
DB	1459	GCTACAGAGTTCTTGAAGTGGTGGCTTAACCTACGGCTACACTAGAAGAACAGTATTGGT	1518						
QY	4114	ATCTGGCTCTGTGAAGCAGGTTACCTTCGGAAGAAAGAGTTGGTAGCTCTTGAATCGGC	4173						
DB	1519	ATCTGGCTCTGTGAAGCAGGTTACCTTCGGAAGAAAGAGTTGGTAGCTCTTGAATCGGC	1578						
QY	4174	AAACAAACACCGCTGGTAGCGGTGTTTTTTTGTGTAAGCAGCAGGATTACCGCGAGA	4233						
DB	1579	AAACAAACACCGCTGGTAGCGGTGTTTTTTTGTGTAAGCAGCAGGATTACCGCGAGA	1638						
QY	4234	AAAAAGGATCTCAAGAGATCTTTTGTATCTTTTCTACGGGGTCTGA-----CG	4282						
DB	1639	AAAAAGGATCTCAAGAGATCTTTTGTATCTTTTCTACGGGGTCTGAAGCTCAGCTAGCG	1698						
QY	4283	CTCAGAGAACTCTGTCAGAGGCGGATAGAAGCGATGCGCTGCGAATTCGGAGCGCGCA	4342						
DB	1699	CTCAGAGAACTCTGTCAGAGGCGGATAGAAGCGATGCGCTGCGAATTCGGAGCGCGCA	1758						

RESULT 5
US-11-186-282-27
; Sequence 27, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: AdviaSys, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response

GENERAL INFORMATION:
; APPLICANT: Advistys, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 2716
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is the codon optimized bovine-GHRH expression plasmid.
US-11-186-282-28

Query Match		32.7%	Score 1771.4;	DB 12;	Length 2716;
Best Local Similarity		98.5%	Pred. No. 0;		
Matches 1802;		Conservative 0;	Mismatches 16;	Indels 11;	Gaps 1;
QY	3454	AGAGGCGGTTTGGGCTATTGGCGCTCTTCCGCTTCTCGCTCACTGACTCGCTCGCGCTCG	3513		
DB	854	AGTGAGGTTAATTTCGAGCTTGGTCTTCCGCTTCTCGCTCACTGACTCGCTCGCGCTCG	913		
QY	3514	GTCTTCGCTGCGGCGAGCGGTATCAGCTCACTCAAGCGGTATATACGGTTATCCACA	3573		
DB	914	GTCTTCGCTGCGGCGAGCGGTATCAGCTCACTCAAGGCGGTAAATACGGTTATCCACA	973		
QY	3574	GAATCAGGGATACCGCAGAAAGACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAC	3633		
DB	974	GAATCAGGGATACCGCAGAAAGACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAC	1033		
QY	3634	CGTAAAAAGCCGCTTGTGCGGCTTTTCCATAGGCTCCGCCCTTCACTGAGCATCAC	3693		
DB	1034	CGTAAAAAGCCGCTTGTGCGGCTTTTCCATAGGCTCCGCCCTTCACTGAGCATCAC	1093		
QY	3694	AAAAATCGACCTCAAGTCAGAGGTGCGGAAACCCGACAGGACTATAAAGATACCAAGCG	3753		
DB	1094	AAAAATCGACCTCAAGTCAGAGGTGCGGAAACCCGACAGGACTATAAAGATACCAAGCG	1153		
QY	3754	TTTTCCCTTGGAGCTCCCTCGCTGCGCTCTCTGTTCCGACCTCGCGCTTACCGGATAC	3813		
DB	1154	TTTTCCCTTGGAGCTCCCTCGCTGCGCTCTCTGTTCCGACCTCGCGCTTACCGGATAC	1213		
QY	3814	CTGTCGCGCTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTAT	3873		
DB	1214	CTGTCGCGCTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTAT	1273		
QY	3874	CTCAGTTCCGTTAGTGTGCTTCCGCTCCAGCTGGGCTGTGTCACGAAACCCCGCTTACG	3933		
DB	1274	CTCAGTTCCGTTAGTGTGCTTCCGCTCCAGCTGGGCTGTGTCACGAAACCCCGCTTACG	1333		
QY	3934	CCGACCGCTGCGCTTATCCGTTAATCTGTTGAGTTCGCTCAACCCGGTTAAGACAGAC	3993		
DB	1334	CCGACCGCTGCGCTTATCCGTTAATCTGTTGAGTTCGCTCAACCCGGTTAAGACAGAC	1393		
QY	3994	TTATCGCCTACGTCAGCAGCCTGGTAAACAGATTAGCAGCGAGGTATGTAGCGGT	4053		
DB	1394	TTATCGCCTACGTCAGCAGCCTGGTAAACAGATTAGCAGCGAGGTATGTAGCGGT	1453		
QY	4054	GCTACAGAGTCTTGAAGTGGTGGCCCTAATACGGCTTACACTAGAGAACAGTATTGGT	4113		
DB	1454	GCTACAGAGTCTTGAAGTGGTGGCCCTAATACGGCTTACACTAGAGAACAGTATTGGT	1513		
QY	4114	ATCTGGCTCTGCTGAAGCCAGTTACTTCGGAAAAAGATTGGTAGCTCTTGAATCCGGC	4173		
DB	1514	ATCTGGCTCTGCTGAAGCCAGTTACTTCGGAAAAAGATTGGTAGCTCTTGAATCCGGC	1573		
QY	4174	AAACAACACCGCTGCTAGCGGTGGTTTTTTTGGTAAAGCAGCAGATTACCGCGAGA	4233		
DB	1574	AAACAACACCGCTGCTAGCGGTGGTTTTTTTGGTAAAGCAGCAGATTACCGCGAGA	1633		
QY	4234	AAAAAAGGATCTCAAGAGATCCTTTTGTATCTTTTCTACGGGGTCTGA-----CG	4282		

DB	1634	AAAAAAGGATCTCAAGAGATCCTTTTGTATCTTTTCTACGGGGTCTGACGCTCAGTAGCG	1693		
QY	4283	CTCAGAAAGAACTCGTCAAGAGCGGATAGAGAGCGATGCGTCCGAATCGGAGCGGCGA	4342		
DB	1694	CTCAGAAAGAACTCGTCAAGAGCGGATAGAGAGCGATGCGTCCGAATCGGAGCGGCGA	1753		
QY	4343	TACCGTAAAGACGAGAGAGCGGTAGCCCATTTCCGCGCAAGCTCTTTCAGCAATATCAC	4402		
DB	1754	TACCGTAAAGACGAGAGAGCGGTAGCCCATTTCCGCGCAAGCTCTTTCAGCAATATCAC	1813		
QY	4403	GGGTAGCCAAACGCTATGTTCTGTATAGCGGTCCGCCACACCCAGCCGGCCACAGTCCGATGA	4462		
DB	1814	GGGTAGCCAAACGCTATGTTCTGTATAGCGGTCCGCCACACCCAGCCGGCCACAGTCCGATGA	1873		
QY	4463	ATCCAGAAAGCGGCCATTTTCCACCATGATATTTCCGCAAGCAGGATCCGCTTGGGTCA	4522		
DB	1874	ATCCAGAAAGCGGCCATTTTCCACCATGATATTTCCGCAAGCAGGATCCGCTTGGGTCA	1933		
QY	4523	CGACGAGATCTCTCGCGTCGCGCATGCGCCCTTGAGCCTGGCGAAACAGTTCGCGTGGCG	4582		
DB	1934	CGACGAGATCTCTCGCGTCGCGCATGCGCCCTTGAGCCTGGCGAAACAGTTCGCGTGGCG	1993		
QY	4583	CGAGCCCTGATGCTCTTCTGTCCAGATCATCTGTATCGACAGACCGGCTTCCATCCGAG	4642		
DB	1994	CGAGCCCTGATGCTCTTCTGTCCAGATCATCTGTATCGACAGACCGGCTTCCATCCGAG	2053		
QY	4643	TACGCTCTCGCTCGATGCGATGTTTCGCTTGGTGGTCAATGGGAGGTAGCCGATCAAA	4702		
DB	2054	TACGCTCTCGCTCGATGCGATGTTTCGCTTGGTGGTCAATGGGAGGTAGCCGATCAAA	2113		
QY	4703	GGGTATGACGCGCGCATTTGCATCAGCCATGATGGATATCTTCTCGGACGAGCAAGGT	4762		
DB	2114	GGGTATGACGCGCGCATTTGCATCAGCCATGATGGATATCTTCTCGGACGAGCAAGGT	2173		
QY	4763	GAGATGACAGGAGATCCTGCCCCCGGCACTTTCGCCCAATAGCAGCAGTCCCTTCCGCTT	4822		
DB	2174	GAGATGACAGGAGATCCTGCCCCCGGCACTTTCGCCCAATAGCAGCAGTCCCTTCCGCTT	2233		
QY	4823	CAGTGACAAAGCTCGACACAGCTGCGCAAGGAAACCGCTGCGGCGGACGACGATAGCC	4882		
DB	2234	CAGTGACAAAGCTCGACACAGCTGCGCAAGGAAACCGCTGCGGCGGACGACGATAGCC	2293		
QY	4883	GGCTGCTCTGCTGCTGAGTTTCAATTCAGGGCACCGGACAGGTCTTTCGACAAAAGAA	4942		
DB	2294	GGCTGCTCTGCTGCTGAGTTTCAATTCAGGGCACCGGACAGGTCTTTCGACAAAAGAA	2353		
QY	4943	CGGGGCGCCCTGCGCTGACAGCCGGAACACCGCGCGCATCAGAGCAGCGATTTGTCTGTT	5002		
DB	2354	CGGGGCGCCCTGCGCTGACAGCCGGAACACCGCGCGCATCAGAGCAGCGATTTGTCTGTT	2413		
QY	5003	GTGCCCAGTCATAGCCGAAATAGCTCTCCACCCAGCGCGCGGAGAACCTTCGCTGCAATC	5062		
DB	2414	GTGCCCAGTCATAGCCGAAATAGCTCTCCACCCAGCGCGCGGAGAACCTTCGCTGCAATC	2473		
QY	5063	CATCTTGTTCATATCATGCGAAACGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	5122		
DB	2474	CATCTTGTTCATATCATGCGAAACGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2533		
QY	5123	TGCGCCATCAGATCTTTCGCGGCAAGAAAGCCATTCAGATTACTTTGAGGGCTTCCCAA	5182		
DB	2534	TGCGCCATCAGATCTTTCGCGGCAAGAAAGCCATTCAGATTACTTTGAGGGCTTCCCAA	2593		
QY	5183	CTTTACAGAGGGCGCCCGCAGCTGGCAATTCGCGTTCGCTGCTGCTTCCATAAAGCGCC	5242		
DB	2594	CTTTACAGAGGGCGCCCGCAGCTGGCAATTCGCGTTCGCTGCTGCTTCCATAAAGCGCC	2653		
QY	5243	AGTCTAGCAACTGTTGGGAAAGGCGGATCG	5271		
DB	2654	AGTCTAGCAACTGTTGGGAAAGGCGGATCG	2682		

US-11-186-282-29
; Sequence 29, Application US/11186282
; Publication No. US20060025369A1
; GENERAL INFORMATION:
; APPLICANT: Advivia, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328, 000265, AVS1-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 2716
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is the codon optimized cat-GHRH expression plasmid.
US-11-186-282-29

Query Match 32.7%; Score 1771.4; DB 12; Length 2716;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1802; Conservative 0; Mismatches 16; Indels 11; Gaps 1;

QY 3454 AGAGGCGTTTGGCTATTGGCGCTCTTTCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 3513
DB 854 AGTGAGGGTTAAATTCAGACTTGGTCTTTCGCTTCCTCGCTCACTGACTCGCTGCGCTCG 913

QY 3514 GTCGTTCCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGCGGTAATACGGTTATCCACA 3573
DB 914 GTCGTTCCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGCGGTAATACGGTTATCCACA 973

QY 3574 GAATCAGGGATACGAGGAAAGAACATGTGAGCAAAAGCCGAGCAAAAGGCGCAGGAAC 3633
DB 974 GAATCAGGGATACGAGGAAAGAACATGTGAGCAAAAGGCGCAGGAAGCCAGGAAGC 1033

QY 3634 CGTAAAGGCGGTTGCGGCTTTTTCATAGGCTCCGCCCTCGCTGAGCGATCATC 3693
DB 1034 CGTAAAGGCGGTTGCGGCTTTTTCATAGGCTCCGCCCTCGCTGAGCGATCATC 1093

QY 3694 AAAAATCGAGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACCAAGCG 3753
DB 1094 AAAAATCGAGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACCAAGCG 1153

QY 3754 TTTCCCTCGAAGCTCCCTGCTGCTCTCTGTTTCGACCTCGCTTTACCGGATAC 3813
DB 1154 TTTCCCTCGAAGCTCCCTGCTGCTCTCTGTTTCGACCTCGCTTTACCGGATAC 1213

QY 3814 CTGTCGCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAAGCTGTAGGTAT 3873
DB 1214 CTGTCGCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAAGCTGTAGGTAT 1273

QY 3874 CTCAGTTGCGGTAGGTGCTTCGCTCCAAAGCTGGGCTGTGTGACAGAACCCCGCTTCAG 3933
DB 1274 CTCAGTTGCGGTAGGTGCTTCGCTCCAAAGCTGGGCTGTGTGACAGAACCCCGCTTCAG 1333

QY 3934 CCCGACCGCTCGGCTTTATCCGGTAACTATGCTTTGAGTCCAAACCCGGTAAAGCAGAC 3993
DB 1334 CCCGACCGCTCGGCTTTATCCGGTAACTATGCTTTGAGTCCAAACCCGGTAAAGCAGAC 1393

QY 3994 TTATCGCCACTGGCAGCAGCCACTGGTAAAGGATTTAGCAGCAGGATGTATAGGCGGT 4053
DB 1394 TTATCGCCACTGGCAGCAGCCACTGGTAAAGGATTTAGCAGCAGGATGTATAGGCGGT 1453

QY 4054 GCTACAGAGTTCTTTGAAGTGGTGGCCTAACTACCGGTACACTAGAGAACAGTATTTGGT 4113
DB 1454 GCTACAGAGTTCTTTGAAGTGGTGGCCTAACTACCGGTACACTAGAGAACAGTATTTGGT 1513

QY 4114 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGAGTTGGTACTTTGATCCGGC 4173
DB 1514 ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGAGTTGGTACTTTGATCCGGC 1573

QY 4174 AAACAAACCCGCTGGTAGCGGTGTTTTTTTGTTCGAAGCAGCAGATTTACGCGAGA 4233
DB 4233

DB 1574 AAACAAACCCGCTGGTAGCGGTGTTTTTTTGTTCGAAGCAGCAGATTTACGCGAGA 1633
QY 4234 AAAAAAGGATCTCAAGAGATCTTTTGATCTTTTCTACGGGGTCTGA-----CG 4282
DB 1634 AAAAAAGGATCTCAAGAGATCTTTTGATCTTTTCTACGGGGTCTGACGCTCAGCTAGTAGCG 1693
QY 4283 CTCAAGAGAACTCGTCAAGAGGCGATAGAAAGCGATGCGCTCGAATCGGGAGCGCGGA 4342
DB 1694 CTCAAGAGAACTCGTCAAGAGGCGATAGAAAGCGATGCGCTCGAATCGGGAGCGCGGA 1753
QY 4343 TACCGTAAAGCACGAGGAAAGCGGTGAGCCCATTCGCGCGCAAGCTCTTTCAGCAATATCAC 4402
DB 1754 TACCGTAAAGCACGAGGAAAGCGGTGAGCCCATTCGCGCGCAAGCTCTTTCAGCAATATCAC 1813
QY 4403 GGGTAGCCAAAGCTATGTCTGTATAGCGGTCCGCCACACCCAGCGCGGCACAGTCGATGA 4462
DB 1814 GGGTAGCCAAAGCTATGTCTGTATAGCGGTCCGCCACACCCAGCGCGGCACAGTCGATGA 1873
QY 4463 ATCCAGAAAGCGGCGCAATTTTCCACATGATATTCGGCAAGCAGGCAATCGCCATGGGTCA 4522
DB 1874 ATCCAGAAAGCGGCGCAATTTTCCACATGATATTCGGCAAGCAGGCAATCGCCATGGGTCA 1933
QY 4523 CGACGAGATCCTCGCGTGGGCAATGCGCGCTTGAGCTTGGCGAAACAGTTTCGGCTGGCG 4582
DB 1934 CGACGAGATCCTCGCGTGGGCAATGCGCGCTTGAGCTTGGCGAAACAGTTTCGGCTGGCG 1993
QY 4583 CGAGCCCCGTATGCTCTTCGTCAGATCATCTTGATCGAACAGACCGGCTTCCATCCGAG 4642
DB 1994 CGAGCCCCGTATGCTCTTCGTCAGATCATCTTGATCGAACAGACCGGCTTCCATCCGAG 2053
QY 4643 TAGTGCTCGCTCGATGCGATGTTTCGTTGGTGGTTCGAATGGCAGGTAGCCCGATCAA 4702
DB 2054 TAGTGCTCGCTCGATGCGATGTTTCGTTGGTGGTTCGAATGGCAGGTAGCCCGATCAA 2113
QY 4703 GCGTATGACGCGCGCATTTGCACTGACGCAATGATGATCTTCTCGGCAAGGCAAGGT 4762
DB 2114 GCGTATGACGCGCGCATTTGCACTGACGCAATGATGATCTTCTCGGCAAGGCAAGGT 2173
QY 4763 GAGTAGCAGGAGATCTGCGCCCGGCACTTTCGCCCATAGCAGCGCTTCCGCTTCCGCTT 4822
DB 2174 GAGTAGCAGGAGATCTGCGCCCGGCACTTTCGCCCATAGCAGCGCTTCCGCTTCCGCTT 2233
QY 4823 CAGTGACAAAGCTCGAGCAAGCTGCGCAAGGAAAGCCCGCTCGTGCCAGCCACCATAGCC 4882
DB 2234 CAGTGACAAAGCTCGAGCAAGCTGCGCAAGGAAAGCCCGCTCGTGCCAGCCACCATAGCC 2293
QY 4883 GCGCTGCTCGTCTGCTGAGTTCATTCAGGGGCAACCGGATCGGTCTTGACAAAAGAA 4942
DB 2294 GCGCTGCTCGTCTGCTGAGTTCATTCAGGGGCAACCGGATCGGTCTTGACAAAAGAA 2353
QY 4943 CCGGCGCCCTGCGCTGACAGCGGGAACCGGCGGATCAGAGCAGCGATTCGCTGTT 5002
DB 2354 CCGGCGCCCTGCGCTGACAGCGGGAACCGGCGGATCAGAGCAGCGATTCGCTGTT 2413
QY 5003 GTGCCAGTCAATAGCCGAATAGCTCTCCACCCAAAGCGGCGGAGAACCTCGCTGCAATC 5062
DB 2414 GTGCCAGTCAATAGCCGAATAGCTCTCCACCCAAAGCGGCGGAGAACCTCGCTGCAATC 2473
QY 5063 CATCTGTTTCAATCATGCGAAACGATCCTCATCTGCTCTTTGATCAGATCTTGATCCCC 5122
DB 2474 CATCTGTTTCAATCATGCGAAACGATCCTCATCTGCTCTTTGATCAGATCTTGATCCCC 2533
QY 5123 TGCGCCATCAGATCTTTGGCGGAAGAAAGCCATCCAGTTTACCTTCAGGGCTTCCCAA 5182
DB 2534 TGCGCCATCAGATCTTTGGCGGAAGAAAGCCATCCAGTTTACCTTCAGGGCTTCCCAA 2593
QY 5183 CTTTACAGAGGGCGCCCGCAGCTGCGCAATTCGCGTTGCTTGTCTCATATAAACCGGCC 5242
DB 2594 CTTTACAGAGGGCGCCCGCAGCTGCGCAATTCGCGTTGCTTGTCTCATATAAACCGGCC 2653
QY 5243 AGTCTAGCAACTGTTGGAAAGGGCGATCG 5271
DB 2654 AGTCTAGCAACTGTTGGAAAGGGCGATCG 2682

QY 5243 AGCTAGCAACTGTTGGAGGCGGATCG 5271
DB |||||||
2654 AGCTAGCAACTGTTGGAGGCGGATCG 2682
|||
RESULT 9
US-11-186-282-26
; Sequence 26, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: Advivys, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 2721
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is the codon optimized pig-GHRH expression plasmid.
US-11-186-282-26
Query Match 32.7%; Score 1771.4; DB 12; Length 2721;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1802; Conservative 0; Mismatches 16; Indels 11; Gaps 1;
QY 3454 AGAGCGGTTGCGTATTGGCGCTCTTCGCGTCTTCCTCGCTCACTGACTCGCTCGCTCG 3513
DB |||||
859 AGTGAGGTTAAATTCAGACTTGGTCTTCGCTTCTCGCTCACTGACTCGCTCGCTCG 918
|||
QY 3514 GTGCTTCGCTGCGCGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGTTATCCACA 3573
DB GTGCTTCGCTGCGCGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGTTATCCACA 978
|||
QY 3574 GAATCAGGGATACCGAGGAAAGCAATGTGACAAAGGCGGAGGCGGAGGCGGAGGCG 3633
DB GAATCAGGGATACCGAGGAAAGCAATGTGACAAAGGCGGAGGCGGAGGCGGAGGCG 1038
|||
QY 3634 CGTAAAGGCGCGTTCGCTGCGCTTTTTCATAGGCTCGCGCCCTCGACGAGCATCAC 3693
DB CGTAAAGGCGCGTTCGCTGCGCTTTTTCATAGGCTCGCGCCCTCGACGAGCATCAC 1098
|||
QY 3694 AAAAATCGAGCTCAAGTACAGAGTGGCGAAACCCGACAGGACTATATAAGATACAGGCG 3753
DB AAAAATCGAGCTCAAGTACAGAGTGGCGAAACCCGACAGGACTATATAAGATACAGGCG 1158
|||
QY 3754 TTTCCCTCGAGCTCCCTCGTGGCTCTCTGTTCCGACCTCGCGCTTACCGGATAC 3813
DB TTTCCCTCGAGCTCCCTCGTGGCTCTCTGTTCCGACCTCGCGCTTACCGGATAC 1218
|||
QY 3814 CTGTCGCTTCTTCCTTCGGAAGGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 3873
DB CTGTCGCTTCTTCCTTCGGAAGGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT 1278
|||
QY 3874 CTCAGTTCCGTTAGGTGCTTCGCTCAAAGTGGGCTGTGTGACAGAACCCCGCTTCAG 3933
DB CTCAGTTCCGTTAGGTGCTTCGCTCAAAGTGGGCTGTGTGACAGAACCCCGCTTCAG 1338
|||
QY 3934 CCGAGCGCTGCGCTTATCGGTAACTATCGTCTTCAGTCCACCCGCTAAGACAGAC 3993
DB CCGAGCGCTGCGCTTATCGGTAACTATCGTCTTCAGTCCACCCGCTAAGACAGAC 1398
|||
QY 3994 TTATCGCACTGGCAGCAGCACTGGTAAACAGGATTAGCAGAGCGGTATGTAGGCGGT 4053
DB TTATCGCACTGGCAGCAGCACTGGTAAACAGGATTAGCAGAGCGGTATGTAGGCGGT 1458
|||
QY 4054 GCTACAGAGTTCTTGAAGTGGTGGCTTAACTACGGCTACACTAGAGAAACAGTATTTGGT 4113
DB GCTACAGAGTTCTTGAAGTGGTGGCTTAACTACGGCTACACTAGAGAAACAGTATTTGGT 1518
|||

QY 4114 ATCTGCGCTCTGCTGAAGCGAGTTACTTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGC 4173
DB |||||||
1519 ATCTGCGCTCTGCTGAAGCGAGTTACTTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGC 1578
|||
QY 4174 AAACAAACCAACCGCTGCTAGCGGTGTTTGTGAAAGCAGAGATACCGCGAGA 4233
DB AAACAAACCAACCGCTGCTAGCGGTGTTTGTGAAAGCAGAGATACCGCGAGA 1638
|||
QY 4234 AAAAAGGATCTCAAGAAGATCTTTGATCTTTTCTACGGGTCTGA-----CG 4282
DB AAAAAGGATCTCAAGAAGATCTTTGATCTTTTCTACGGGTCTGACCGTCTAGCTAGCG 1698
|||
QY 4283 CTCAGAAGAACTCGTCAAGAAGCGGATAGAAAGCGATGCGCTGCGAATCGGGAGCGCGA 4342
DB CTCAGAAGAACTCGTCAAGAAGCGGATAGAAAGCGGATGCGCTGCGAATCGGGAGCGCGA 1758
|||
QY 4343 TACCGTAAAGCACGAGGAAAGCGTCAAGCCATTCGCGCGCAAGCTCTTTCAGCAATATCAC 4402
DB TACCGTAAAGCACGAGGAAAGCGGTCAAGCCATTCGCGCGCAAGCTCTTTCAGCAATATCAC 1818
|||
QY 4403 GGGTAGCAACGCTATGTCTGATAGCGGTCCGCCACACCCGCGGCGCACAGTCCGATGA 4462
DB GGGTAGCAACGCTATGTCTGATAGCGGTCCGCCACACCCGCGGCGCACAGTCCGATGA 1878
|||
QY 4463 ATCCAGAAAGCGGCCAATTTCCACCATGATATTCGCGAAGCAGGATCCGCATGGGTCA 4522
DB ATCCAGAAAGCGGCCAATTTCCACCATGATATTCGCGAAGCAGGATCCGCATGGGTCA 1938
|||
QY 4523 CGACGAGATCCTCGCGTGGGCGATGCGCGCTTGAGCCTTGGCGAAACAGTTTCGGCTGGCG 4582
DB CGACGAGATCCTCGCGTGGGCGATGCGCGCTTGAGCCTTGGCGAAACAGTTTCGGCTGGCG 1998
|||
QY 4583 CGAGCCCTGATGCTCTTCGTCAGATCATCTCGATCGAACAGACCGGCTTCATCCGAG 4642
DB CGAGCCCTGATGCTCTTCGTCAGATCATCTCGATCGAACAGACCGGCTTCATCCGAG 2058
|||
QY 4643 TAGCTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTTCGAAATGGGCGAGTAGCCGATCAA 4702
DB TAGCTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTTCGAAATGGGCGAGTAGCCGATCAA 2118
|||
QY 4703 GCGTATGACGCGCGGATTTGCAATCAGCCATGATGGAATCTTTCTCGGCAAGGCAAGGT 4762
DB GCGTATGACGCGCGGATTTGCAATCAGCCATGATGGAATCTTTCTCGGCAAGGCAAGGT 2178
|||
QY 4763 GAGTGAAGAGATCTGCGCCCGGCACTTCGCGCCCAATAGCAGCAGTCCCTTCCCGCTT 4822
DB GAGTGAAGAGATCTGCGCCCGGCACTTCGCGCCCAATAGCAGCAGTCCCTTCCCGCTT 2238
|||
QY 4823 CAGTGAACAAGCTCGAGCACAGCTGCGCAAGGAAACGCCCGTTCGTGGCCAGACGATAGCC 4882
DB CAGTGAACAAGCTCGAGCACAGCTGCGCAAGGAAACGCCCGTTCGTGGCCAGACGATAGCC 2298
|||
QY 4883 GCGCTGCTCCTCGTCAAGTTCAATTCAGGGCAACCGGACAGGTGCTTTCGAAAAAGAA 4942
DB GCGCTGCTCCTCGTCAAGTTCAATTCAGGGCAACCGGACAGGTGCTTTCGAAAAAGAA 2358
|||
QY 4943 CCGGCGCCCTGCGCTGACAGCGGAAACAGCGGCGATCAGAGCAGCGGATTCGCTGTT 5002
DB CCGGCGCCCTGCGCTGACAGCGGAAACAGCGGCGATCAGAGCAGCGGATTCGCTGTT 2418
|||
QY 5003 GTGCCAGTCTATAGCGGAATAGCTCTCCACCAAGCGCGGAGAACCTTCGCTGCAATC 5062
DB GTGCCAGTCTATAGCGGAATAGCTCTCCACCAAGCGCGGAGAACCTTCGCTGCAATC 2478
|||
QY 5063 CATCTTGTTCATCATGCGAAAAAGATCCTCATCTGCTCTTGTGATCAGATCTTGATCCCC 5122
DB CATCTTGTTCATCATGCGAAAAAGATCCTCATCTGCTCTTGTGATCAGATCTTGATCCCC 2538
|||
QY 5123 TGGCCCATCAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTCAGGGCTTCCAA 5182
DB TGGCCCATCAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTCAGGGCTTCCAA 2598
|||
QY 5183 CCTTACAGAGGCGCGCCCGAGCTGGCAATTTCCGGTTTCGCTTGTGCTCCATAAAACCGCCC 5242
|||


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Db 2599 CCTTACAGAGGCGCCAGCTGGCAATTCGCGTTTCGCTGCTCCATAAAACCGCCC 2658
Qy 5243 AGTCTAGCAACTGTTGGGAAGGCGGATCG 5271
Db 2659 AGTCTAGCAACTGTTGGGAAGGCGGATCG 2687

RESULT 10
US-11-186-282-34
; Sequence 34, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: Advisys, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVSI-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34
; LENGTH: 2721
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is the codon optimized Human-GHRH expression plasmid.
US-11-186-282-34

Query Match 32.7%; Score 1771.4; DB 12; Length 2721;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1802; Conservative 0; Mismatches 16; Indels 11; Gaps 1;

Qy 3454 AGAGGCGGTGTTGGGTATGCGGCTCTTCGGCTTCCTCGCTCACTGACTCGCTCGCTCG 3513
Db 859 AGTAGGGTTAATTCAGAGTTGGTCTTCGGCTTCCTCGCTCACTGACTCGCTCGCTCG 918

Qy 3514 GTCGTTTCGGTGGCGAGCGGTATCAGTCACTCAAGCGGTAAATACGGTTATCCACA 3573
Db 919 GTCGTTTCGGTGGCGAGCGGTATCAGTCACTCAAGCGGTAAATACGGTTATCCACA 978

Qy 3574 GAATCAGGGGTAACCGAGGAAGACATGTGAGCAAAAGGCCAGAAAGCCAGGAAC 3633
Db 979 GAATCAGGGGTAACCGAGGAAGACATGTGAGCAAAAGGCCAGAAAGCCAGGAAC 1038

Qy 3634 CGTAAAGCGCGCTGCTGGCGTTTTCATAGGCTCGCGCCCTCGACGAGCATAC 3693
Db 1039 CGTAAAGCGCGCTGCTGGCGTTTTCATAGGCTCGCGCCCTCGACGAGCATAC 1098

Qy 3694 AAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAAGCG 3753
Db 1099 AAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAAGCG 1158

Qy 3754 TTTCCCGCTGGAAGCTCCCTCGCGCTCTCTGTTTCGACCCCTGCGCTTACCGGATAC 3813
Db 1159 TTTCCCGCTGGAAGCTCCCTCGCGCTCTCTGTTTCGACCCCTGCGCTTACCGGATAC 1218

Qy 3814 CTGTCGCGCTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCAAGCTGTAGGTAT 3873
Db 1219 CTGTCGCGCTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCAAGCTGTAGGTAT 1278

Qy 3874 CTCAGTTCGGTGTAGTGTGCTTCGCTCAAGCTGGGCTGTGTGACGAACCCCGCTTCAG 3933
Db 1279 CTCAGTTCGGTGTAGTGTGCTTCGCTCAAGCTGGGCTGTGTGACGAACCCCGCTTCAG 1338

Qy 3934 CCGACCGCTGCGCTTATTCGGTAACTATCTGTTGAGTCCACCCGTTAAGACAGAC 3993
Db 1339 CCGACCGCTGCGCTTATTCGGTAACTATCTGTTGAGTCCACCCGTTAAGACAGAC 1398

Qy 3994 TTATGCCCACTGCGACGACCACTGTGTAAAGATTAGCAGCGGAGGTATGTAGCGGT 4053
Db 1399 TTATGCCCACTGCGACGACCACTGTGTAAAGATTAGCAGCGGAGGTATGTAGCGGT 1458

Qy 4054 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAGAAGACAGTATTGGT 4113

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Db 1459 GCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAGAAGACAGTATTGGT 1518
Qy 4114 ATCTGCGCTCTGCTGAAGCCAGTTACTTTCGAAAAAGAGTTGTTAGTCTTTCATCCGGC 4173
Db 1519 ATCTGCGCTCTGCTGAAGCCAGTTACTTTCGAAAAAGAGTTGTTAGTCTTTCATCCGGC 1578
Qy 4174 AAACAAACACCGCTGTTAGCGGTGTTTTTTTGTGTTGCAAGCAGCAGATTACCGCAGA 4233
Db 1579 AAACAAACACCGCTGTTAGCGGTGTTTTTTTGTGTTTAAAGCAGCAGATTACCGCAGA 1638
Qy 4234 AAAAAGGATCTCAAGAAGATCTTTTGTATCTTTTCTACGGGTCTGA-----CG 4282
Db 1639 AAAAAGGATCTCAAGAAGATCTTTTGTATCTTTTCTACGGGTCTGACGCTCAGTAGCG 1698
Qy 4283 CTCAGAAGAACTCGTCAAGAAGCGATAGAAGCGATCGCTCGCAATCGGGAGCGCGCA 4342
Db 1699 CTCAGAAGAACTCGTCAAGAAGCGATAGAAGCGATCGCTCGCAATCGGGAGCGCGCA 1758
Qy 4343 TACCGTAAAGCAGCAGGAAGCGGTCAAGCCCATTTGCGCGCCAAAGCTCTTCAGCAATATCAC 4402
Db 1759 TACCGTAAAGCAGCAGGAAGCGGTCAAGCCCATTTGCGCGCCAAAGCTCTTCAGCAATATCAC 1818
Qy 4403 GGGTAGCCAAACGCTATGCTCTGATAGCGGTTCGCGCAACCCAGCCCGCCACAGTCTGATGA 4462
Db 1819 GGGTAGCCAAACGCTATGCTCTGATAGCGGTTCGCGCAACCCAGCCCGCCACAGTCTGATGA 1878
Qy 4463 ATCCAGAAAGCGGCCATTTTCCACCATGATATTCGGAAGCAGGATCGCCATGGGTCA 4522
Db 1879 ATCCAGAAAGCGGCCATTTTCCACCATGATATTCGGAAGCAGGATCGCCATGGGTCA 1938
Qy 4523 CGACGAGATCTTCGCGCTCGCGCATGCGCGCTTGAAGCTTGGCGAAACAGTTCGGCTGGCG 4582
Db 1939 CGACGAGATCTTCGCGCTCGCGCATGCGCGCTTGAAGCTTGGCGAAACAGTTCGGCTGGCG 1998
Qy 4583 CGAGCCCTGATGCTCTTCGTCAGATCATCTGATGCAAGACCGGCTTCCATCCGAG 4642
Db 1999 CGAGCCCTGATGCTCTTCGTCAGATCATCTGATGCAAGACCGGCTTCCATCCGAG 2058
Qy 4643 TACGTCTCGCTCGATGCGATGTTTCGTTGGTGGTTCGAATGGCGAGGTAGCCGATCAA 4702
Db 2059 TACGTCTCGCTCGATGCGATGTTTCGTTGGTGGTTCGAATGGCGAGGTAGCCGATCAA 2118
Qy 4703 GGGTATGACGCGCGCATTTGCTATGAGCTATGATGATATTTCTCGGAGGAGCAAGGT 4762
Db 2119 GGGTATGACGCGCGCATTTGCTATGAGCTATGATGATATTTCTCGGAGGAGCAAGGT 2178
Qy 4763 GAGATGACAGGAGATCTTCGCGCGCATTTGCGCCCAATAGCAGCAGTCTTCCTCCGCTT 4822
Db 2179 GAGATGACAGGAGATCTTCGCGCGCATTTGCGCCCAATAGCAGCAGTCTTCCTCCGCTT 2238
Qy 4823 CAGTGAACAGTCGAGCAGCTGCGCAAGGAACCGCGCTGCGGAGCAGCAGTAGCC 4882
Db 2239 CAGTGAACAGTCGAGCAGCTGCGCAAGGAACCGCGCTGCGGAGCAGCAGTAGCC 2298
Qy 4883 GCGCTGCTCTGCTGCGATTTCAATTCAGGCGCACCGGACAGGTCGCTTTCGACAAAAGAA 4942
Db 2299 GCGCTGCTCTGCTGCGATTTCAATTCAGGCGCACCGGACAGGTCGCTTTCGACAAAAGAA 2358
Qy 4943 CCGGCGCGCTTCGCTGCTGACCGGAAACACCGCGCATCAGAGCAGCGATTTGCTGTT 5002
Db 2359 CCGGCGCGCTTCGCTGCTGACCGGAAACACCGCGCATCAGAGCAGCGATTTGCTGTT 2418
Qy 5003 GTGCGCAGTCATAGCGGATAGCTCTCCACCAAGCGCGCGGAGAACCTGCGTGAATC 5062
Db 2419 GTGCGCAGTCATAGCGGATAGCTCTCCACCAAGCGCGCGGAGAACCTGCGTGAATC 2478
Qy 5063 CATCTGTTCAATCATGCGAAACGATCTCTATCTCTCTTGTATCAGATCTTGTATCCCC 5122
Db 2479 CATCTGTTCAATCATGCGAAACGATCTCTATCTCTCTTGTATCAGATCTTGTATCCCC 2538
Qy 5123 TCGGCGCATCAGATCTTCGCGCGCAAGAAAGCCATCCAGTTTACTTTTGCAGGGCTTCCCAA 5182

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Db 2539 TGGCCATCAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTCAGGGCTTCCCAA 2598
Qy 5183 CTTTACAGAGGGCGCCCGCCAGCTGGCAATTCGGTTTCGGTTCTGCTTCCATAAACCGCC 5242
Db 2599 CTTTACAGAGGGCGCCCGCCAGCTGGCAATTCGGTTTCGGTTCTGCTTCCATAAACCGCC 2658
Qy 5243 AGTCTAGCAACTGTTGGGAAGGCGGATCG 5271
Db 2659 AGTCTAGCAACTGTTGGGAAGGCGGATCG 2687

RESULT 11
US-11-186-282-25
; Sequence 25, Application US/11186282
; Publication No. US20060025368A1
; GENERAL INFORMATION:
; APPLICANT: Advivys, Inc.
; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response
; FILE REFERENCE: 108328.000265 AVS1-0042
; CURRENT APPLICATION NUMBER: US/11/186,282
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 2725
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is the codon optimized HV-GHRH expression plasmid.
US-11-186-282-25

Query Match 32.7%; Score 1771.4; DB 12; Length 2725;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1802; Conservative 0; Mismatches 16; Indels 11; Gaps 1;

Qy 3454 AGAGGGGTTTGGGTATTGGCGCTCTTCGGCTTCTCGCTCACTCACTCGCTCGCTCG 3513
Db 863 AGTGGGGTTAAATTCGAGCTTGGTCTTCGGCTTCTCGCTCACTCACTCGCTCGCTCG 922
Qy 3514 GTCTTGGCTGGCGGAGCGGTATCAGCTCATCAAGGCGGTATATACGGTTATCCACA 3573
Db 923 GTCTTGGCTGGCGGAGCGGTATCAGCTCATCAAGGCGGTATATACGGTTATCCACA 982
Qy 3574 GAATCAGGGATTAACGAGAAAGACATGTGAGCAAAAGCCAGCAAAAGCCGAGAAC 3633
Db 983 GAATCAGGGGATTAACGAGAAAGACATGTGAGCAAAAGCCAGCAAAAGCCGAGAAC 1042
Qy 3634 CGTAAAGGCGCGTTCCTGGCGTTCCTATAGGCTCCGCGCCCTCGACGAGCATCAC 3693
Db 1043 CGTAAAGGCGCGTTCCTGGCGTTCCTATAGGCTCCGCGCCCTCGACGAGCATCAC 1102
Qy 3694 AAAATCGACCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACGAGCG 3753
Db 1103 AAAATCGACCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACGAGCG 1162
Qy 3754 TTTCCCGCTCGAGCTCCCTCGCTCGCTCTCTGTTCCGACCTCGCGCTTACCGGATAC 3813
Db 1163 TTTCCCGCTCGAGCTCCCTCGCTCGCTCTCTGTTCCGACCTCGCGCTTACCGGATAC 1222
Qy 3814 CTGTCCCGCTTCTCCCTTCGGGAAGCGTGGCGTTCCTATAGCTCACCGCTGTAGGTAT 3873
Db 1223 CTGTCCCGCTTCTCCCTTCGGGAAGCGTGGCGTTCCTATAGCTCACCGCTGTAGGTAT 1282
Qy 3874 CTAGTTTCGTGTAGGTTCGTTCGATCCAAAGTGGGTGTGTGACGAAACCCCGCTTCAG 3933
Db 1283 CTAGTTTCGTGTAGGTTCGTTCGATCCAAAGTGGGTGTGTGACGAAACCCCGCTTCAG 1342
Qy 3934 CCGACCGCTCGCGCTTATCCGGTAACTATTCGTTCCAGTCCACCCGCTTAAGACAGAC 3993
Db 1343 CCGACCGCTCGCGCTTATCCGGTAACTATTCGTTCCAGTCCACCCGCTTAAGACAGAC 1402
Qy 3994 TTATCGCACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGCGAGGTATGTAGGCGGT 4053
Db

Db 1403 TTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGAGCGAGGTATGTAGGCGGT 1462
Qy 4054 GCTACAGAGTCTTTCGAAGTGGTGGCTTAACCTACGGCTACACTAGAGAAGACAGATTATGGT 4113
Db 1463 GCTACAGAGTCTTTCGAAGTGGTGGCTTAACCTACGGCTACACTAGAGAAGACAGATTATGGT 1522
Qy 4114 ATCTGCGCTCTCTGCTGAAGCCAGTTACCTTCGGAAGAAAGAGTTGGTAGCTCTTTCGATCCGGC 4173
Db 1523 ATCTGCGCTCTCTGCTGAAGCCAGTTACCTTCGGAAGAAAGAGTTGGTAGCTCTTTCGATCCGGC 1582
Qy 4174 AAACAAACCAACCGCTGTAGCGGTGTTTTTTTGGTAAAGCAGAGATTAGCCGAG 4233
Db 1583 AAACAAACCAACCGCTGTAGCGGTGTTTTTTTGGTAAAGCAGAGATTAGCCGAG 1642
Qy 4234 AAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTCA-----CG 4282
Db 1643 AAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGCTAGCG 1702
Qy 4283 CTCAAGAAATCTCTCAAGAAGCCGATAGAAGCGATGCGCTGCGAATCGGAGCGCGGA 4342
Db 1703 CTCAAGAAATCTCTCAAGAAGCCGATAGAAGCGATGCGCTGCGAATCGGAGCGCGGA 1762
Qy 4343 TACCGTAAAGCAGAGAGAGCGGTCAAGCCATTCGCGGCAAGCTCTTCAGCAATATCAC 4402
Db 1763 TACCGTAAAGCAGAGAGAGCGGTCAAGCCATTCGCGGCAAGCTCTTCAGCAATATCAC 1822
Qy 4403 GGGTAGCCAAACGCTATGTCTGATAGCGGTTCGCGCACACCCAGCGGCCACAGTCGATGA 4462
Db 1823 GGGTAGCCAAACGCTATGTCTGATAGCGGTTCGCGCACACCCAGCGGCCACAGTCGATGA 1882
Qy 4463 ATCCAGAAAGCGGCCATTTTCCACCATGATATTTCGCAAGCAGGATCGCCATGGGTCA 4522
Db 1883 ATCCAGAAAGCGGCCATTTTCCACCATGATATTTCGCAAGCAGGATCGCCATGGGTCA 1942
Qy 4523 CGACGAGATCTCTCGCTCGGCGATGCGCGCTTTGAGCCCTGGCGAAGAGTTTCGGTGGCG 4582
Db 1943 CGACGAGATCTCTCGCTCGGCGATGCGCGCTTTGAGCCCTGGCGAAGAGTTTCGGTGGCG 2002
Qy 4583 CGAGCCCTGTAGTCTCTGTCAGATCATCTGTATCGAAGCAAGACCGGCTTCCATCCGAG 4642
Db 2003 CGAGCCCTGTAGTCTCTGTCAGATCATCTGTATCGAAGCAAGACCGGCTTCCATCCGAG 2062
Qy 4643 TAGTGTCTGCTCGATCGATGTTTCGCTTGGTGGTTCGAATGGCGAGGTAGCCGATCAA 4702
Db 2063 TAGTGTCTGCTCGATCGATGTTTCGCTTGGTGGTTCGAATGGCGAGGTAGCCGATCAA 2122
Qy 4703 GCGTATGACGCGCGCGGATTTGCAATGAGCATCTTCTGCGCAGGAGCAAGGT 4762
Db 2123 GCGTATGACGCGCGCGGATTTGCAATGAGCATCTTCTGCGCAGGAGCAAGGT 2182
Qy 4763 GAGTACAGAGGATCTGCGCCCGGCACTTCGCCCAATAGCAGCAGTCCCTTCCCGCTT 4822
Db 2183 GAGTACAGAGGATCTGCGCCCGGCACTTCGCCCAATAGCAGCAGTCCCTTCCCGCTT 2242
Qy 4823 CAGTGACAGCTCGACACAGCTGCGCAAGAAAGCGCGCTGGCGCAGCACGATAGCC 4882
Db 2243 CAGTGACAGCTCGACACAGCTGCGCAAGAAAGCGCGCTGGCGCAGCACGATAGCC 2302
Qy 4883 GCGTGTCTGCTCGTTCAGGTCATTTCAGGGCAACCGGACAGGTGCTTTCAGCAAAAGAA 4942
Db 2303 GCGTGTCTGCTCGTTCAGGTCATTTCAGGGCAACCGGACAGGTGCTTTCAGCAAAAGAA 2362
Qy 4943 CCGGCGCGCTCGCTGACAGCGCGGAAACACGCGGCATCAGAGCAGCCGATGTCTGTT 5002
Db 2363 CCGGCGCGCTCGCTGACAGCGCGGAAACACGCGGCATCAGAGCAGCCGATGTCTGTT 2422
Qy 5003 GTGCCAGTCAATAGCGGAATAGCTCTTCCACCAAGCGCGCGGAGAACCTTCGCTGAATC 5062
Db 2423 GTGCCAGTCAATAGCGGAATAGCTCTTCCACCAAGCGCGCGGAGAACCTTCGCTGAATC 2482
Qy 5063 CATCTTGTTCATATGCGGAAACGATCTCTCATCTGCTTCTGATCAGATCTTGATCCCC 5122
Db 2483 CATCTTGTTCATATGCGGAAACGATCTCTCATCTGCTTCTGATCAGATCTTGATCCCC 2542

Qy	5063	CATCTTGTTCAATCATCGAAGCATCCTCATCTCTGTCCTCTTGATCAGATCTTGATCCCC	5122
Db	2483	CATCTTGTTCAATCATCGAAGCATCCTCATCTCTGTCCTCTTGATCAGATCTTGATCCCC	2542
Qy	5123	TGGGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTGACGGGCTTCCAA	5182
Db	2543	TGGGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTGACGGGCTTCCAA	2602
Qy	5183	CCTTACACAGAGGGGCCCCAGCTGGCAATTCGGTTGCGTTGCTGTGCCATAAAACCGCCC	5242
Db	2603	CCTTACACAGAGGGGCCCCAGCTGGCAATTCGGTTGCGTTGCTGTGCCATAAAACCGCCC	2662
Qy	5243	AGTCTAGCAACTGTTGGGAAGGGCGATCG	5271
Db	2663	AGTCTAGCAACTGTTGGGAAGGGCGATCG	2691

RESULT 13

US-11-186-282-30

; Sequence 30, Application US/11186282

; Publication No. US20060025368A1

; GENERAL INFORMATION:

; APPLICANT: Advlyse, Inc.

; TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response

; FILE REFERENCE: 108328.000265 AVSI-0042

; CURRENT APPLICATION NUMBER: US/11/186,282

; CURRENT FILING DATE: 2005-07-21

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 30

; LENGTH: 2739

; TYPE: DNA

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: This is the codon optimized TI-GHRH expression plasmid.

US-11-186-282-30

3934	Qy	CCGACCGCTGCGCCTTATCTCCGCTAACTATCTGCTTGGATGTCACACCCGGTAAACACACGAC	3993
1357	Db	CCGACCGCTGCGCCTTATCTCCGCTAACTATCTGCTTGGATGTCACACCCGGTAAACACACGAC	1416
3994	Qy	TTATCGCCACTGCGACGAGCCACTGCTTAAACAGGATTTAGCAGCGAGGATGATGTAGCGCGT	4053
1417	Db	TTATCGCCACTGCGACGAGCCACTGCTTAAACAGGATTTAGCAGCGAGGATGATGTAGCGCGT	1476
4054	Qy	GCTACAGAGTTCTTGAAGTGGTGGCTTAACTACCGGCTACACTAGAAAGAACAGATTTTGGT	4113
1477	Db	GCTACAGAGTTCTTGAAGTGGTGGCTTAACTACCGGCTACACTAGAAAGAACAGATTTTGGT	1536
4114	Qy	ATCTGCGCTCTGCTGAAGCCAGTTACTCTTCGGAAGAAAGAGTTGGTAGCTCTTGATCCGGC	4173
1537	Db	ATCTGCGCTCTGCTGAAGCCAGTTACTCTTCGGAAGAAAGAGTTGGTAGCTCTTGATCCGGC	1596
4174	Qy	AAACAAACACCGCTGTGTAGCGGTGGTTTTTTTTTTTGTGCAAGCAGCAGAGATTACGCGCAGA	4233
1597	Db	AAACAAACACCGCTGTGTAGCGGTGGTTTTTTTTTTTGTGCAAGCAGCAGAGATTACGCGCAGA	1656
4234	Qy	AAAAAGGATCTCAAGAAGATCTCTTTGATCTTTTCTACGGGGTCTGA-----CG	4282
1657	Db	AAAAAGGATCTCAAGAAGATCTCTTTGATCTTTTCTACGGGGTCTGAAGCTCAGCTAGCG	1716
4283	Qy	CTCAGAAGAACTCTGCTCAAGAAGCGGATAGAAAGCGGATCGCTCGGAATTCGGAGACGGCGA	4342
1717	Db	CTCAGAAGAACTCTGCTCAAGAAGCGGATAGAAAGCGGATCGCTCGGAATTCGGAGACGGCGA	1776
4343	Qy	TACGTTAAGCAGAGGAGCGGTGACGCCATTCGGCGCCCAAGCTCTTCAGCAATATCAC	4402
1777	Db	TACGTTAAGCAGAGGAGCGGTGACGCCATTCGGCGCCCAAGCTCTTCAGCAATATCAC	1836
4403	Qy	GGGTAGCCAAACGCTATGTCTCTGATAGCGGTCCGCCACACCCAGCCCGGCCACAGTCGATGA	4462
1837	Db	GGGTAGCCAAACGCTATGTCTCTGATAGCGGTCCGCCACACCCAGCCCGGCCACAGTCGATGA	1896
4463	Qy	ATCCAGAAAAGCGGCCATTTTCCCAATGATATTCGGCAAGCAGGCAATGCCATNGGTCA	4522
1897	Db	ATCCAGAAAAGCGGCCATTTTCCCAATGATATTCGGCAAGCAGGCAATGCCATNGGTCA	1956
4523	Qy	CGACGAGATCCTCGCCGTGGGCATCGCGCCTTGAGCCTGGCGACAGTTCCGCTGGCG	4582
1957	Db	CGACGAGATCCTCGCCGTGGGCATCGCGCCTTGAGCCTGGCGACAGTTCCGCTGGCG	2016
4583	Qy	CGAGCCCTCATGCTCTTCGTCCAGATCATCTCTGATCGACAAGACCGGCTTCATCCGAG	4642
2017	Db	CGAGCCCTCATGCTCTTCGTCCAGATCATCTCTGATCGACAAGACCGGCTTCATCCGAG	2076
4643	Qy	TACGTGCTCGCTCGATGCGATGTTTCGTGTGGTGGATGGCAATGGCAGGTTAGCCGATCAA	4702
2077	Db	TACGTGCTCGCTCGATGCGATGTTTCGTGTGGTGGATGGCAATGGCAGGTTAGCCGATCAA	2136
4703	Qy	CGGTATGACCGCGCATTTGATCAGCCATGATGATATCTTTCTCGGCAGGAGCAAGGT	4762
2137	Db	CGGTATGACCGCGCATTTGATCAGCCATGATGATATCTTTCTCGGCAGGAGCAAGGT	2196
4763	Qy	GAGATGACAGGAGATCTCTGCCCGGCACATTCGCCCAATAGCAGCAGTCCCTTCCCGCTT	4822
2197	Db	GAGATGACAGGAGATCTCTGCCCGGCACATTCGCCCAATAGCAGCAGTCCCTTCCCGCTT	2256
4823	Qy	CAGTGACACCGTGGAGCAGACTGCGCAAGGAACGCCCGCTCGTGGCCAGCCAGATAGCC	4882
2257	Db	CAGTGACACCGTGGAGCAGACTGCGCAAGGAACGCCCGCTCGTGGCCAGCCAGATAGCC	2316
4883	Qy	CGGCTGCTCTGCTCTGAGTTCAATTACGGGCAACCGGACAGGTGCGTCTTGACAAAAAGAA	4942
2317	Db	CGGCTGCTCTGCTCTGAGTTCAATTACGGGCAACCGGACAGGTGCGTCTTGACAAAAAGAA	2376
4943	Qy	CCGGCGCCCTCGGCTGACAGCGGGAACACGGCGCATCAGAGCAGCCGATGCTGT	5002
2377	Db	CCGGCGCCCTCGGCTGACAGCGGGAACACGGCGCATCAGAGCAGCCGATGCTGT	2436
5003	Qy	GTGCCCAAGTCAAGCCGAATAGCTCTCTCCACCAAGCGCGGAGAACCTTGGCGTCAATC	5062

Db 2437 GTGCCAGTATAGCCCTCTCCACCCAGCGCGGAGAACCTCGCTGCAATC 2496
 Qy 5063 CATCTTGTCAATCATCGAAACGATCCTCATCTCTCTTGTATCAGATCTTGTATCCCC 5122
 Db 2497 CATCTTGTCAATCATCGAAACGATCCTCATCTCTCTTGTATCAGATCTTGTATCCCC 2556
 Qy 5123 TGGCCATCAGATCTTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGACGGCTTCCCAA 5182
 Db 2557 TGGCCATCAGATCTTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGACGGCTTCCCAA 2616
 Qy 5183 CCTTACAGAGGCGCGCCAGCTGGCAATTCGGTTCTGCTTGTCTCATAAACCGCCC 5242
 Db 2617 CCTTACAGAGGCGCGCCAGCTGGCAATTCGGTTCTGCTTGTCTCATAAACCGCCC 2676
 Qy 5243 AGTCTAGCAACTGTTGGGAAGGCGATCG 5271
 Db 2677 AGTCTAGCAACTGTTGGGAAGGCGATCG 2705

RESULT 14

US-10-523-682-1/c
 ; Sequence 1, Application US/10523682
 ; Publication No. US20060014149A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schorr, Kirk
 ; TITLE OF INVENTION: Methods for rolling circle amplification and signal trapping of
 ; FILE OF INVENTION: libraries
 ; FILE REFERENCE: 10292.204-US
 ; CURRENT APPLICATION NUMBER: US/10/523.682
 ; CURRENT FILING DATE: 2005-02-01
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 1
 ; LENGTH: 2403
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Plasmid pMHas5
 US-10-523-682-1

Query Match 25.3%; Score 1372.8; DB 7; Length 2403;
 Best Local Similarity 82.4%; Pred. No. 0;
 Matches 1759; Conservative 0; Mismatches 172; Indels 203; Gaps 8;
 Qy 3269 TTCTGTGTGAATTTGTTATCCGCTCACAATTCACACACATACGAGCGGAGCATAA 3328
 Db 2193 TTCTGTGTGAATTTGTTATCCGCTCACAATTCACACACATACGAGCGGAGCATAA 2134
 Qy 3329 AGTGTAAAGCTGGGTGCTTAATGAGTGAGCTAACTCACATTAATTTGCGTTGCGTCC 3388
 Db 2133 AGTGTAAAGCTGGGTGCTTAATGAGTGAGCTAACTCACATTAATTTGCGTTGCGTCC 2074
 Qy 3389 TGGCGGTTTCAGTGGGAAACCTGTGTCGAGCTGATTAATGATCGGCAACGCG 3448
 Db 2073 TGGCGGTTTCAGTGGGAAACCTGTGTCGAGCTGATTAATGATCGGCAACGCG 2014
 Qy 3449 CGGGAGAGCGGTTTTCGCTATTGGGCGCTTCCGCTTCTCGCTCAGTCTCGCTGC 3508
 Db 2013 CGGGAGAGCGGTTTTCGCTATTGGGCGCTTCTCGCTTCTCGCTCAGTCTCGCTGC 1954
 Qy 3509 GCTCGGTTTCGCTGCGGAGCGGTATCAGCTCACTCAAAAGGCGGTAAATCGGTTAT 3568
 Db 1953 GCTCGGTTTCGCTGCGGAGCGGTATCAGCTCACTCAAAAGGCGGTAAATCGGTTAT 1894
 Qy 3569 CCACAGATCAGGGATTAACGCGAGGAAGAACATGTGAGCAAAAGGCCACGAAAGGCCA 3628
 Db 1893 CCACAGATCAGGGATTAACGCGAGGAAGAACATGTGAGCAAAAGGCCACGAAAGGCCA 1863
 Qy 3629 GGAACGTAAAGGCGCGTTGCTGCGCTTTTCCATAGGCTCCGCCCTCGACGAGC 3688
 Db 1862 -----GGCAAGCGGTTTTCATAGGCTCCGCCCTCGACGAGC 1822

Qy 3689 ATCAAAAAATCGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACC 3748
 Db 1821 ATCAAAAAATCGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACC 1762
 Qy 3749 AGCGGTTTCCCGCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTCGCGCTTACCG 3808
 Db 1761 AGCGGTTT-CCCGTGGCGCTCCCTCGTGGCTCTCTGTTCCGCTTTCGCTTACCG 1703
 Qy 3809 GATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTA 3868
 Db 1702 G-----TGTCAATTCGCGCTTATGGCGCGTGTGTCTCATTCACGC-----C 1660
 Qy 3869 GGTATCTCAGTTCGCTGAGTCTGCTTCGCTCAAGCTGGCTGTGTGCAAGAACCCCG 3928
 Db 1659 TGACACTCAGTTCGCGGTAGGCAAGTTCGCTTCAAGCTGGACTGTATGACGAACCCCG 1600
 Qy 3929 TTCAGCCCGACCGCTGGCTTATCCGCTTAACCTATCGTCTTGAGTCCAAACCCGTAAGAC 3988
 Db 1599 TTCAGTCCGACCGCTGGCTTATCCGCTTAACCTATCGTCTTGAGTCCAAACCCGTAAGAC 1540
 Qy 3989 ACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGAGCGAGGTATGTAG 4048
 Db 1539 ATGCAAAAGCACCACCTGGCAGCAGCCACTGGTAAATTTAGTATAGGAGTTAG----- 1488
 Qy 4049 GCGGTGCTACAGAGTTCCTGAACTGCTGCTTAACTACGCTACACTAGAGAACAGTAT 4108
 Db 1487 -----TCTTGAAGTCAATGCGCGCTTAAAGCTTAACTGAAAGGACAAAGTT 1443
 Qy 4109 TTGGTATCGCGCTCTGTGNAAGCCAGTTTACCTTCGGAAGAAAGAGTTGGTGTCTTGAT 4168
 Db 1442 TTGGTACTGCGCTCTCTC-CAAGCCAGTTTACCTCGGTTCAAGAGTTGGTGTCTCAGAGA 1384
 Qy 4169 CCGGCAAAACAAACACCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 4228
 Db 1383 ACCTTCGAAAACCGCGCTGCAAGCGGT-TTTTTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1326
 Qy 4229 GCAGAAAAAAGGATCTCAAGAAAGATCTTTTGATCTTTTCTA----- 4270
 Db 1325 GCAGACCAAAACGATCTCAAGAAAGATCATCTTATTAATCAGATAAAATATTTCTAGATTT 1266
 Qy 4271 ----- 4270
 Db 1265 CAGTGCAATTTATCTCTCAAAATGTAGCACCTGAAGTCAGCCCATACGATATAAGTTGT 1206
 Qy 4271 -----CGGGTCTGACGCTCAGAACCCAGAGTCCCGCTCAGAGAGACTCGT 4297
 Db 1205 AATTCATGTTTGACAGCTTATCATCGGAAACCCAGAGTCCCGCTCAGAGAGACTCGT 1146
 Qy 4298 CAAGAAAGCGATAGAAAGCGATGCGCTGCGAATTCGGGAGCGCGGATACCGTAAAGCACGA 4357
 Db 1145 CAAGAAAGCGATAGAAAGCGATGCGCTGCGAATTCGGGAGCGCGGATACCGTAAAGCACGA 1086
 Qy 4358 GGNAGCGGTGAGCCCAATTCGCGCCCAAGCTCTTCAGCAATATCAGCGGTAGCCAAAGCTTA 4417
 Db 1085 GGAAGCGGTGAGCCCAATTCGCGCCCAAGCTCTTCAGCAATATCAGCGGTAGCCAAAGCTTA 1026
 Qy 4418 TGTCTGTAGTAGCGGTCCGCGCACACCCAGCGCGGCGCAGTGTGAATTCAGAAAGCGGC 4477
 Db 1025 TGTCTGTAGTAGCGGTCCGCGCACACCCAGCGCGGCGCAGTGTGAATTCAGAAAGCGGC 966
 Qy 4478 CATTTTCCACCATGATATTTCGCAAGCAGGCAATCGCCATCGGCTCAGAGATCTCTCG 4537
 Db 965 CATTTTCCACCATGATATTTCGCAAGCAGGCAATCGCCATCGGCTCAGAGATCTCTCG 906
 Qy 4538 CGTGGGCGATGCGCGCTTGGCTGGCGAAACGTTTGGCTGGCGGAGCCCTCGTGTCT 4597
 Db 905 CGTGGGCGATGCGCGCTTGGCTGGCGAAACGTTTGGCTGGCGGAGCCCTCGTGTCT 846
 Qy 4598 CTTTGTCCAGATCATCTGATCGACAAAGACCGGCTTCCATCCGAGTACGTCTCGCTCGA 4657
 Db 845 CTTTGTCCAGATCATCTGATCGACAAAGACCGGCTTCCATCCGAGTACGTCTCGCTCGA 786
 Qy 4658 TGCATGTTTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 4717

[illegible]

RESULT 15

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US-11-094-484-3/c
; Sequence 3, Application US/11094484
; Publication No. US20050261231A1
; GENERAL INFORMATION:
; APPLICANT: KUBO, TATEKI
; APPLICANT: TANAG, MARVIN A.
; APPLICANT: YANO, KENJI
; APPLICANT: HOSOKAWA, KO
; APPLICANT: MORISHITA, RYUICHI
; TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR NUCLEIC ACID SEQUENCE TO
; TITLE OF INVENTION: ENHANCE MUSCULOCUTANEOUS FLAP SURVIVAL
; FILE REFERENCE: 074257-0108
; CURRENT APPLICATION NUMBER: US/11/094,484
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: 60/557,835
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 3
; LENGTH: 5181
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: vector sequence
US-11-094-484-3
Query Match          24.8%   Score 1347.2;   DB 12;   Length 5181;

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Db 4161 CGAATCGGAGCGCGATACCGTAAAGACACAGAGAAAGCGGTGAGCCCATTCGCCGCCAAG 4102
 QY CTCTTCAGCAATATCACGGGTAGTACCAACGCTATGTCTCTGATAGCGGTCCGCCACACCCAG 4445
 Db 4101 CTCTTCAGCAATATCACGGGTAGTACCAACGCTATGTCTCTGATAGCGGTCCGCCACACCCAG 4042
 QY CCGGCCACAGTCGATGAATCCAGAAAGCGGCCATTTCCACCATGATATTCGGCAAGCA 4505
 Db 4041 CCGGCCACAGTCGATGAATCCAGAAAGCGGCCATTTCCACCATGATATTCGGCAAGCA 3982
 QY GGCATCGCCATGGTACGACGAGATCCTCGCGTGGGCGATGGCGCCTTGAGCCTGGC 4565
 Db 3981 GGCATCGCCATGGTACGACGAGATCCTCGCGTGGGCGATGGCGCCTTGAGCCTGGC 3922
 QY GAAACAGTTCGGCTGGCGGAGCCCTGATGCTCTTCGTCCAGATCATCTCTGATCGACAAG 4625
 Db 3921 GAACAGTTCGGCTGGCGGAGCCCTGATGCTCTTCGTCCAGATCATCTCTGATCGACAAG 3862
 QY ACCGGCTTCATCCGAGTACGTCGCTCGATGCGATGTTTCGTTGGTGGTGAATGG 4685
 Db 3861 ACCGGCTTCATCCGAGTACGTCGCTCGATGCGATGTTTCGTTGGTGGTGAATGG 3802
 QY GCAGGTAGCCGATCAAGCGTATGACGCGCCGATTCGATCAGCCATGATGGATATCTTT 4745
 Db 3801 GCAGGTAGCCGATCAAGCGTATGACGCGCCGATTCGATCAGCCATGATGGATATCTTT 3742
 QY CTCGGCAGGACGAAGGTGAGTACAGAGAGATCTCGCCCGGCACTTCGCCCAATAGCAG 4805
 Db 3741 CTCGGCAGGACGAAGGTGAGTACAGAGAGATCTCGCCCGGCACTTCGCCCAATAGCAG 3682
 QY CCAGTCCCTTCCCGCTTCACTGAGCAACGTCGAGCAGCTGCGCAAGGAACGCCGCTGT 4865
 Db 3681 CCAGTCCCTTCCCGCTTCACTGAGCAACGTCGAGCAGCTGCGCAAGGAACGCCGCTGT 3622
 QY GGCAGGCACGATAGCGCGCTGCTCTGCTGAGTTCATTTCAGGGCAGCGACAGGTC 4925
 Db 3621 GGCAGGCACGATAGCGCGCTGCTCTGCTGAGTTCATTTCAGGGCAGCGACAGGTC 3562
 QY GGTCTTGACAAAAGAACCGGGCGCCCTGCGCTGACAGCGGGAACACGCGCGCATCAGA 4985
 Db 3561 GGTCTTGACAAAAGAACCGGGCGCCCTGCGCTGACAGCGGGAACACGCGCGCATCAGA 3502
 QY GCAGCCGATGTCTGTTGTGCCAGTCATAGCCGAATAGCCTCTCCACCCCAAGCGGCCG 5045
 Db 3501 GCAGCCGATGTCTGTTGTGCCAGTCATAGCCGAATAGCCTCTCCACCCCAAGCGGCCG 3442
 QY AGAACCTGCGTCAATCCATCTTGTTCATCATGCGAAGAGATCCTCATCTCTCTTGG 5105
 Db 3441 AGAACCTGCGTCAATCCATCTTGTTCATCATGCGAAGAGATCCTCATCTCTCTTGG 3382
 QY ATCAGATCTTTGATCCCTCGCCATCAGATCCTTGGCGCAAGAAAGCCATCCAGTTTAC 5165
 Db 3381 ATCAGATCTTTGATCCCTCGCCATCAGATCCTTGGCGCAAGAAAGCCATCCAGTTTAC 3322
 QY TTTCAGGGCTTCCCAACCTTACAGAGGGCGCCCAAGCTGGCAATTCGGTTTCGCTTGC 5225
 Db 3321 TTTCAGGGCTTCCCAACCTTACAGAGGGCGCCCAAGCTGGCAATTCGGTTTCGCTTGC 3262
 QY TGTCCATAAAACCGCCAGT 5245
 Db 3261 TGTCCATAAAACCGCCAGT 3242

Search completed: February 20, 2006, 19:49:16
 Job time : 1300 secs

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Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_NA_Main) and **.rapbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 18:48:03 ; Search time 25985 Seconds
(without alignments)
11863.076 Million cell updates/sec

Title: US-10-798-896-1

Perfect score: 5423

Sequence: 1 ccaccgcgtggcgccgtc.....ctataggcgaattggagct 5423

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 2842172563 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

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3: gb.env.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	5423	100.0	5423	6	CQ877110 Sequence
2	2237	41.3	2237	6	CQ877114 Sequence
3	2218	40.9	3599	6	BD063790 Insulin-1
4	2218	40.9	3599	6	BD069041 Treatment
5	2218	40.9	3803	6	CQ877111 Sequence
6	2215.8	40.9	3600	6	BD063789 Insulin-1
7	2215.8	40.9	3600	6	BD069040 Treatment
8	2211.6	40.8	3558	6	CQ854738 Sequence
9	2160	39.8	3534	6	CQ854723 Sequence
10	2160	39.8	3534	6	CQ854724 Sequence
11	2160	39.8	3534	6	CQ854725 Sequence
12	2160	39.8	3534	6	CQ854726 Sequence
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14	2160	39.8	3534	6	CQ854741 Sequence
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17	2160	39.8	3534	6	CQ903783 Sequence
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19	2160	39.8	3534	6	CQ903785 Sequence
20	2160	39.8	3534	6	CS131823 Sequence
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22	1989	36.7	4496	6	AX249945 Sequence
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ALIGNMENTS

RESULT 1
CQ877110
LOCUS CQ877110 5423 bp DNA linear PAT 04-OCT-2004
DEFINITION Sequence 1 from Patent WO2004081040.
ACCESSION CQ877110
VERSION CQ877110.1 GI:53790386

KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Rabinovsky, E.D. and Draghia-Akli, R.
TITLE Insulin-like growth factor (igf-i) plasmid-mediated supplementation for therapeutic applications

JOURNAL Patent: WO 2004081040-A 1 23-SEP-2004;
FEATURES Advsys, Inc. (US); BAYLOR COLLEGE OF MEDICINE (US)
Location/Qualifiers
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/note="Nucleic acid sequence for the pAV2001 plasmid."

ORIGIN

Query Match 100.0%; Score 5423; DB 6; Length 5423;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 CCACCGCGTGGCGCGCTCGCCCTCGGCACCATCTCAGCACACCCAAATATGGCGAC 60
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DB 61 GGGTGAGGAATGTGGGGAGTTATTTTAGAGCGGTGAGGAGGTGGCGGCGGACGAGT 120
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RESULT 2
CQ877114
LOCUS CQ877114 2237 bp DNA linear PAT 04-OCT-2004
DEFINITION Sequence 5 from Patent WO2004081040.
ACCESSION CQ877114
VERSION CQ877114.1 GI:53790389
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Rabinovsky,E.D. and Draghia-Akli,R.
TITLE Insulin-like growth factor (igf-i) plasmid-mediated supplementation

for therapeutic applications
Patent: WO 2004081040-A 5 23-SBP-2004;
Adviseys, Inc. (US); BAYLOR COLLEGE OF MEDICINE (US)
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DEFINITION
BD063790 3599 bp DNA linear PAT 27-AUG-2002
Insulin-like growth factor I (IGF)-1 expression system and methods
of use.
ACCESSION
BD063790
VERSION
BD063790.1 GI:22609393
KEYWORDS
JP 2001505435-A/3.
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 3599)
AUTHORS
Coleman,M., Schwartz,R. and Demayo,F.J.
TITLE
Insulin-like growth factor I (IGF)-1 expression system and methods
of use.
JOURNAL
Patent: JP 2001505435-A 3 24-APR-2001;
BARENTIS INC,BAYLOR COLLEGE OF MEDICINE
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PN JP 2001505435-A/3
PD 24-APR-2001
PF 01-DEC-1997 JP 1998525696
PR 02-DEC-1996 US 60/031539,19-NOV-1997 US 08/974572 PI
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RESULT 4			
BD069041			
LOCUS			
DEFINITION Treatment for urinary incontinence using gene therapy techniques.			
ACCESSION BD069041			
VERSION BD069041.1 GI:22614644			

RESULT 4
BD069041
LOCUS
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ACCESSION
VERSION

KEYWORDS JP 2001511154-A/3.
SOURCE unidentified
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REFERENCE 1 (bases 1 to 3599)
AUTHORS Coleman,M. for urinary incontinence using gene therapy techniques
TITLE Treatment: JP 2001511154-A 3 07-AUG-2001;
JOURNAL BARENTIS INC
COMMENT OS Unidentified
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RESULT 7
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LOCUS BD069040 3600 bp DNA linear PAT 27-AUG-2002
DEFINITION Treatment for urinary incontinence using gene therapy techniques.
ACCESSION BD069040
VERSION BD069040.1 GI:22614643
KEYWORDS JP 2001511154-A/2.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 3600)
AUTHORS Coleman,M.
TITLE Treatment for urinary incontinence using gene therapy techniques
JOURNAL Patent: JP 2001511154-A 2 07-AUG-2001;
BARENTIS INC
COMMENT OS Unidentified
PN JP 2001511154-A/2
PD 07-AUG-2001
PF 04-FEB-1998 JP 1998533206
PR 04-FEB-1997 US 60/036862
PI MICHAEL COLEMAN
PC A61K48/00
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Topology: Linear;
CC Treatment for urinary incontinence using gene therapy CC
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RESULT 8
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LOCUS CQ854738 3558 bp DNA linear PAT 23-AUG-2004
DEFINITION Sequence 26 from Patent WO2004067719.
ACCESSION CQ854738
VERSION CQ854738.1 GI:51510298
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Brown, P. A., Draghia-Akli, R. and Carpenter, R. H.
TITLE Reducing culling in herd animals growth hormone releasing hormone (ghrh)
JOURNAL Patent: WO 2004067719-A 26 12-AUG-2004;
Adviseys, Inc. (US)
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Best Local Similarity 99.5%; Pred. No. 0;
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LOCUS CQ854723 3534 bp DNA linear PAT 23-AUG-2004
DEFINITION Sequence 11 from Patent WO2004067719.
ACCESSION CQ854723
VERSION CQ854723.1 GI:51510283
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Brown, P.A., Draghia-Akli, R. and Carpenter, R.H.
TITLE Reducing culling in herd animals growth hormone releasing hormone (ghrh)
JOURNAL Patent: WO 2004067719-A 11 12-AUG-2004;
Advisys, Inc. (US)
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Best Local Similarity 99.5%; Pred. No. 0;
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other sequences; artificial sequences.
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AUTHORS Brown,P.A., Draghia-Akli,R. and Carpenter,R.H.
TITLE Reducing culling in herd animals growth hormone releasing hormone(ghrh)
JOURNAL Patent: WO 2004067719-A 12 12-AUG-2004;
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PAT 23-AUG-2004


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AUTHORS Draghia-Akli, R., Scott, C. and Brown, P. A.
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1	5423	100.0	5423	13	ADS73973 Plasmid p
2	4958.2	91.4	5707	2	AAX88055 Plasmid p
3	2785.8	51.4	6345	2	AAX88054 Plasmid p
4	2237	41.3	2237	13	ADS73977
5	2218	40.9	3599	2	AAV50428 Plasmid p
6	2218	40.9	3599	2	AAV40796 Actual se
7	2218	40.9	3803	13	ADS73974 Plasmid p
8	2215.8	40.9	3600	2	AAV50427 Plasmid p
9	2215.8	40.9	3600	2	AAV40795
10	2211.6	40.8	3558	9	AAL60457
11	2211.6	40.8	3558	13	ADR23406
12	2160	39.8	2192	6	ABQ78294 Nucleotid
13	2160	39.8	3534	6	ABQ78293 Nucleotid
14	2160	39.8	3534	9	AAL62060 TV-GHRH p
15	2160	39.8	3534	9	AAL62062 Wild-type
16	2160	39.8	3534	9	AAL62059 TI-GHRH p
17	2160	39.8	3534	9	AAL62058 pSP-HV-GH
18	2160	39.8	3534	9	AAL62061 15/27/28-
19	2160	39.8	3534	9	AAL60444 TI-GHRH p

20	2160	39.8	3534	9	AAL60445
21	2160	39.8	3534	9	AAL60446
22	2160	39.8	3534	9	AAL60443
23	2160	39.8	3534	9	AAL60447
24	2160	39.8	3534	10	ACF04661
25	2160	39.8	3534	10	ACF04660
26	2160	39.8	3534	10	ACF04657
27	2160	39.8	3534	10	ACF04659
28	2160	39.8	3534	10	ACF04658
29	2160	39.8	3534	12	ADF90306
30	2160	39.8	3534	12	ADF90302
31	2160	39.8	3534	12	ADF90304
32	2160	39.8	3534	12	ADF90305
33	2160	39.8	3534	12	ADF90303
34	2160	39.8	3534	12	ADL70452
35	2160	39.8	3534	12	ADL70453
36	2160	39.8	3534	12	ADL70454
37	2160	39.8	3534	12	ADO31099
38	2160	39.8	3534	12	ADO31100
39	2160	39.8	3534	12	ADO31098
40	2160	39.8	3534	12	ADO31101
41	2160	39.8	3534	13	ADR23409
42	2160	39.8	3534	13	ADR23393
43	2160	39.8	3534	13	ADR23394
44	2160	39.8	3534	13	ADR23395
45	2160	39.8	3534	13	ADR23392

ALIGNMENTS

RESULT 1

ADS73973

ID ADS73973 standard; DNA; 5423 BP.

XX ADS73973;

DT 16-DEC-2004 (first entry)

DE Plasmid pAV2001 nucleotide sequence.

XX IGF-I; insulin-like growth factor I; myogenic promoter; MEF-1; MEF-2;
TEF-1; SRE; SP; alpha actin; growth hormone; angiogenesis; myogenesis;
KW vascular endothelial growth factor; VEGF; VEGF receptor; anti-diabetic;
KW cardiant; vasotropic; ophthalmological; cerebroprotective; ds.
XX Synthetic.
XX WO2004081040-A2.
XX 23-SEP-2004.
XX 11-MAR-2004; 2004WO-US007295.
XX 12-MAR-2003; 2003US-0454079P.
XX (ADVI-) ADVISYS INC.
XX (BAYU) BAYLOR COLLEGE MEDICINE.
XX Rabinovsky ED, Draghia-Akli R;
XX WPI; 2004-668935/65.
XX New isolated nucleic acid expression construct having a myogenic
PT promoter, a nucleic acid sequence encoding IGF-I, and a 3'UTR, useful
PT for treating diabetes, ischemic heart and cerebrovascular disease.
XX Claim 11; SEQ ID NO 1; 104pp; English.
XX The invention relates to an isolated nucleic acid expression construct
CC comprising a myogenic promoter, a nucleic acid sequence encoding an
CC insulin-like growth factor I (IGF-I) or its functional biological
CC equivalent, and a 3' untranslated region (3'UTR), which has in vivo

3961	Qy	TATCGCTTCAGTCCAAACCCGGTAAGACA	CGACTTATTCGCCACTTGGCAGCAGCACTGGT	4020
3961	Db	TATCGCTTCAGTCCAAACCCGGTAAGACA	CGACTTATTCGCCACTTGGCAGCAGCACTGGT	4020
4021	Qy	AAACAGATTAGCAGCGCAGGTATGTAGGCGGTGCTACAGAGTTCTTTGAAGTGGTGGCCT	4080	
4021	Db	AAACAGATTAGCAGCGCAGGTATGTAGGCGGTGCTACAGAGTTCTTTGAAGTGGTGGCCT	4080	
4081	Qy	AACTACGGCTPACACTAGAAGAAACAGTATTTGGTATCTGCGCTCTGCTGGAAGCCAGTTTACC	4140	
4081	Db	AACTACGGCTPACACTAGAAGAAACAGTATTTGGTATCTGCGCTCTGCTGGAAGCCAGTTTACC	4140	
4141	Qy	TTCCGAAAAAGATTTGGTAGCTCTTGATCCGGCAAAACAAACCCGCTGGTAGCGGTGGT	4200	
4141	Db	TTCCGAAAAAGATTTGGTAGCTCTTGATCCGGCAAAACAAACCCGCTGGTAGCGGTGGT	4200	
4201	Qy	TTTTTTTGTTCGAAGCAGCAGATTTACCGGCAGAAAAAAGGATCTCAAGAAGATCCTTTTG	4260	
4201	Db	TTTTTTTGTTCGAAGCAGCAGATTTACCGGCAGAAAAAAGGATCTCAAGAAGATCCTTTTG	4260	
4261	Qy	ATCTTTTCTACGGGCTCTGACGCTCAGAAGAACTCGTCAAGAAAGCGGATAGAAAGGCGATG	4320	
4261	Db	ATCTTTTCTACGGGCTCTGACGCTCAGAAGAACTCGTCAAGAAAGCGGATAGAAAGGCGATG	4320	
4321	Qy	CGCTGCGAATCGGAGCGGCGATACCGTAAGACA	CGAGGAAGCGGTCAGGCCATTTGCGCG	4380
4321	Db	CGCTGCGAATCGGAGCGGCGATACCGTAAGACA	CGAGGAAGCGGTCAGGCCATTTGCGCG	4380
4381	Qy	CCAAAGCTCTTCAGCAATATCACGGGTAGCCAAACGCTATGTCCTGTATAGCGGTGGCGCAC	4440	
4381	Db	CCAAAGCTCTTCAGCAATATCACGGGTAGCCAAACGCTATGTCCTGTATAGCGGTGGCGCAC	4440	
4441	Qy	CCACGCGGCCACACAGTCGATGAATCCAGAAAAAGCGGCATTTTCCACCATGATATTCGGC	4500	
4441	Db	CCACGCGGCCACACAGTCGATGAATCCAGAAAAAGCGGCATTTTCCACCATGATATTCGGC	4500	
4501	Qy	AAGCAGGCATCGCCATGGGTACAGACAGAGATCTCTGCGCGTCGGGCATCGCGCCTTGAGC	4560	
4501	Db	AAGCAGGCATCGCCATGGGTACAGACAGAGATCTCTGCGCGTCGGGCATCGCGCCTTGAGC	4560	
4561	Qy	CTGGCGAAAGTTTCGGCTGGCGGAGCGCCCTGATGCTCTTCGTGCAGATCATCTGTATCG	4620	
4561	Db	CTGGCGAAAGTTTCGGCTGGCGGAGCGCCCTGATGCTCTTCGTGCAGATCATCTGTATCG	4620	
4621	Qy	ACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTTCGCTGGTGGTTCG	4680	
4621	Db	ACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTTCGCTGGTGGTTCG	4680	
4681	Qy	AATGGGCAGGTAGCCGGATCAAGCGTATGACGCGCGCGCATTTGCATCAGCCATGATGGAT	4740	
4681	Db	AATGGGCAGGTAGCCGGATCAAGCGTATGACGCGCGCGCATTTGCATCAGCCATGATGGAT	4740	
4741	Qy	ACTTTCTCGGACGAGAGCAAGGTGAGATGACAGGAGATCTGCGCCCGGCACTTTGGCCCAAT	4800	
4741	Db	ACTTTCTCGGACGAGAGCAAGGTGAGATGACAGGAGATCTGCGCCCGGCACTTTGGCCCAAT	4800	
4801	Qy	AGCAGCCAGTCCCTTCCCGCTTACGTGACAAACGTCGAGCA	CAGCTGCGCAAGGAACGCC	4860
4801	Db	AGCAGCCAGTCCCTTCCCGCTTACGTGACAAACGTCGAGCA	CAGCTGCGCAAGGAACGCC	4860
4861	Qy	GTCTGCGCCAGCCACGATAGCCGCGCTGCTCTGCTCGATGTTTCAATTCAGGGCACCGGAC	4920	
4861	Db	GTCTGCGCCAGCCACGATAGCCGCGCTGCTCTGCTCGATGTTTCAATTCAGGGCACCGGAC	4920	
4921	Qy	AGGTCGGTCTTGACAAAAAGAAACCGGGCGCCCTTGCGCTGACAGCCGGAAACCGGGCGCA	4980	
4921	Db	AGGTCGGTCTTGACAAAAAGAAACCGGGCGCCCTTGCGCTGACAGCCGGAAACCGGGCGCA	4980	
4981	Qy	TCAGACAGCCGATGTTGCTGTTGTCAGTATAGCCGATAGCTCTCCACCCCAAGCG	5040	
4981	Db	TCAGACAGCCGATGTTGCTGTTGTCAGTATAGCCGATAGCTCTCCACCCCAAGCG	5040	
5041	Qy	GCCGGAAACCTGCGTGGCAATCCATCTGTTTCAATCATGCGAAACGATCTCATCTCTGTC	5100	

[illegible]

Diseases that can be treated include muscle atrophy associated with neurological, muscular or systemic disease, aging by causing tissues to express trophic factors, haemophilia by causing tissues to express and secrete clotting factor into the circulation, atherosclerosis and atherosclerotic cardiovascular, cerebrovascular or peripheral-vascular disease by causing tissues to express factors involved in tissue metabolism. They can be used to replace genes of inherited genetic defects or acquired hormone deficiencies e.g. diabetes. To transform cells to produce particular proteins or RNA in vitro. To create transgenic animals which can be used for research into human diseases, assessing novel therapeutic methods, assessing the effect of chemical and physical carcinogens and for studying the effect of genes and genetic regulatory elements or livestock improvement. They can be used to induce an immune response. These vectors provide controlled expression of the genes they carry and produce a significantly high level of expression. Using 3'UTR sequences reduces the decay rates of the mRNAs encoded by the vectors which causes increased expression

XX Sequence 5707 BP; 1221 A; 1634 C; 1576 G; 1276 T; 0 U; 0 Other;

Query Match 91.4%; Score 4958.2; DB 2; Length 5707;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 5007; Conservative 0; Mismatches 4; Indels 37; Gaps 1;

413 CCATGGGAAAATCAGCAGTCTTCCAAACCCAAATTTAAGTGTGCTTTTGTGATTTCT 472
414 CCATGGGAAAATCAGCAGTCTTCCAAACCCAAATTTAAGTGTGCTTTTGTGATTTCT 706
473 TGAAGTGAAGATGCACACATGCTCTCTCGCATCTTCTACCTGGCGCTGCTGCG 532
707 TGAAGTGAAGATGCACACATGCTCTCTCGCATCTTCTACCTGGCGCTGCTGCG 766
533 TCACCTTCACAGCTCTGCGCACCGCTGACCGAGAGCGCTCTCGGGGGCTGAGCTGGTG 592
767 TCACCTTCACAGCTCTGCGCACCGCTGACCGAGAGCGCTCTCGGGGGCTGAGCTGGTG 826
593 ATGCTCTTCAAGTGTGTGTGAGACAGGGGCTTTTATTTCACAAAGCCACAGGGTATG 652
827 ATGCTCTTCAAGTGTGTGTGAGACAGGGGCTTTTATTTCACAAAGCCACAGGGTATG 886
653 GCTCCAGAGTCCGAGGGGCGCTCAGACAGGTATCTGGATGATGCTGCTTCGGAGCT 712
887 GCTCCAGAGTCCGAGGGGCGCTCAGACAGGTATCTGGATGATGCTGCTTCGGAGCT 946
713 GTGATCTTAAGAGGCTGGAGATGTATTGCGCACCCCTCAAGCTCGCAAGTCAAGCTCGCT 772
947 GTGATCTTAAGAGGCTGGAGATGTATTGCGCACCCCTCAAGCTCGCAAGTCAAGCTCGCT 1006
773 CTGTCCGTGCCAGCGCCACACCGACATGCCAAGACCCCAAGAGGAAGTACATTTGAAGA 832
1007 CTGTCCGTGCCAGCGCCACACCGACATGCCAAGACCCCAAGAGGAAGTACATTTGAAGA 1066
833 ACCGAGTACAGGAGTGCAGGAAACAGAACTACAGGATGTAGGAGACCCCTCTGAGG 892
1067 ACCGAGTACAGGAGTGCAGGAAACAGAACTACAGGATGTAGGAGACCCCTCTGAGG 1126
893 AGTGAAGAGTGCATGCCAGGAGTCCCGGGGCTGAGGAAATTCGATGCGCCATCC 952
1127 AGTGAAGAGTGCATGCCAGGAGTCCCGGGGCTGAGGAAATTCGATGCGCCATCC 1186
953 ATTGTCCACCGTAAATGCTTTCTAAACATGTTTACATGATCACTTTGCGCAACCACTCAG 1012
1187 ATTGTCCACCGTAAATGCTTTCTAAACATGTTTACATGATCACTTTGCGCAACCACTCAG 1246
1013 GATGACAAATCTGTAGGTTCCAGGCTGCTGAGGACCTTCCACGACCAATGCAACTTTCTAT 1072
1247 GATGACAAATCTGTAGGTTCCAGGCTGCTGAGGACCTTCCACGACCAATGCAACTTTCTAT 1306
1073 TTTGTGAACAATTTCTGGTTACTGTGCTGCAAGAGCTCCATGTCACAGGTATGTAAG 1132
1307 TTTGTGAACAATTTCTGGTTACTGTGCTGCAAGAGCTCCATGTCACAGGTATGTAAG 1366
1133 TGTACATAAATAAATTTATTTTACCTCGTTTGTGTTGTTTTTAAACCAATGCGCTGTGG 1192

1367 TGTACATAAATAAATTTATTTTACCTCGTTTGTGTTTGTGTTTTTAAACCAATGCGCTGTGG 1426
1193 AAGGAAACATAAAATCTTCAAGAGCATTAATCATCAGTCATTCGTGCACACCCCTAATG 1252
1427 AAGGAAACATAAAATCTTCAAGAGCATTAATCATCAGTCATTCGTGCACACCCCTAATG 1486
1253 CAGTTGTTTCTGTGCATCATTTCCCTGGGCTTTCCATCTCTCGCTGACCTGGGAGCTGGT 1312
1487 CAGTTGTTTCTGTGCATCATTTCCCTGGGCTTTCCATCTCTCGCTGACCTGGGAGCTGGT 1546
1313 GCTGGGGCTGGGAGCAGGGGTTGGGGCTCTCCAGGAGAGATGGCATGGGAGAGTCAATG 1372
1547 GCTGGGGCTGGGAGCAGGGGTTGGGGCTCTCCAGGAGAGATGGCATGGGAGAGTCAATG 1606
1373 GGATACCTGCTGGGGGGGGGGGACTCACCTCTGCTGGGCTGCAGGAGAGCCCATTTGGTGCA 1432
1607 GGATACCTGCTGGGGGGGGGGGACTCACCTCTGCTGGGCTGCAGGAGAGCCCATTTGGTGCA 1666
1433 GAGAGCAGCTGGGATGCCCATGACACGGGACCCACTGCAACCGTGTCTTCCCATGCC 1492
1667 GAGAGCAGCTGGGATGCCCATGACACGGGACCCACTGCAACCGTGTCTTCCCATGCC 1726
1493 AGTAGGAAAGGTTACGAGCGCGTTTCACTCTCAGCTTGTGAAGGATTTTGTGGGCTC 1552
1727 AGTAGGAAAGGTTACGAGCGCGTTTCACTCTCAGCTTGTGAAGGATTTTGTGGGCTC 1786
1553 AGCTCCAGAGCAGTAGCAGGATGCTGTCAGCTCCGAGCTCGAGTGTGAGAGGATTTTGGGAGC 1612
1787 AGCTCCAGAGCAGTAGCAGGATGCTGTCAGCTCCGAGCTCGAGTGTGAGAGGATTTTGGGAGC 1846
1613 AAGGCTGCAGCTGAGGCGCAGGTTGGGCA CAGGTTAAATTAAGAGCTTTCCATCCACT 1672
1847 AAGGCTGCAGCTGAGGCGCAGGTTGGGCA CAGGTTAAATTAAGAGCTTTCCATCCACT 1906
1673 TATGAAAGGCTCTCTGCACTCACCCTGTCCCTGGGGCTGGGGGAGCAGGAGGCACTTC 1732
1907 TATGAAAGGCTCTCTGCACTCACCCTGTCCCTGGGGCTGGGGGAGCAGGAGGCACTTC 1966
1733 CTCACCCCACTGCACACAAAGGCTTTGCTGCACACGAGGACCTCTCTGTGGGCCACAGA 1792
1967 CTCACCCCACTGCACACAAAGGCTTTGCTGCACACGAGGACCTCTCTGTGGGCCACAGA 2026
1793 CTCTTATAGATTCGCTGTGCCCTTAGGAGAC CAGGGGGCTTTCCCTGCTGGCCCTTCTGGC 1852
2027 CTCTTATAGATTCGCTGTGCCCTTAGGAGAC CAGGGGGCTTTCCCTGCTGGCCCTTCTGGC 2086
1853 CCGGGGACACCTGCAGGAGCTGCCCTATCTGCCCTCTCTTAGATGCTCTGGCAGGAGG 1912
2087 CCGGGGACACCTGCAGGAGCTGCCCTATCTGCCCTCTCTTAGATGCTCTGGCAGGAGG 2146
1913 CTGCATCTGGCTTTGGGGCTGATCCATATTACCTGAGTGCAGTGCAGGAGCAGTCTGTGAAG 1972
2147 CTGCATCTGGCTTTGGGGCTGATCCATATTACCTGAGTGCAGTGCAGGAGCAGTCTGTGAAG 2206
1973 AAAAGATGATTTTCAACTGAACTTACTATCCAGGAGGTTTATTCCTTTATTTGATGGTG 2032
2207 AAAAGATGATTTTCAACTGAACTTACTATCCAGGAGGTTTATTCCTTTATTTGATGGTG 2266
2033 CTAAGAGTGGCTTTTCTCTCACTGTAAATGATTTTGGCTCATGTGTGAATACACTTTCCA 2092
2267 CTAAGAGTGGCTTTTCTCTCACTGTAAATGATTTTGGCTCATGTGTGAATACACTTTCCA 2326
2093 ATAAAGCAGCAGCTCCAAAGGAAATTTCTGAGGAGAGACAGTACTCTGTGTGGGAAG 2152
2327 ATAAAGCAGCAGCTCCAAAGGAAATTTCTGAGGAGAGACAGTACTCTGTGTGGGAAG 2386
2153 TCCTCTGAGAGGCTTATGCTTCAAGCTGAAATGGCTGGGACTGGCTGGGAGAGCAGGAT 2212
2387 TCCTCTGAGAGGCTTATGCTTCAAGCTGAAATGGCTGGGACTGGCTGGGAGAGCAGGAT 2446
2213 CACATCCTTTTAAAGACAAACAGAGGTAGTGTGACCTTGTGTTTATTTACTATT 2272

2447 CACATCCCTTTTAAAGACAAACAGAGGTAGTGTGACCTTGTGTAATTAATAATT 2506
2273 TAGCGTGTGTTCTCAGTGACAATACCTCAACGGGGATATGAGAGCTATTTCCCAAC 2332
2507 TAGCGGTGTGTTTCAAGTGACAATACCTCAACGGGGATATGAGAGCTATTTCCCAAC 2566
2333 CCTCGCTGCTGGACCCCTGATCTGGGGTTTTCCGTAGCTTTAAGCGGTGCCAACTGCTTAA 2392
2567 CCTCGCTGCTGGACCCCTGATCTGGGGTTTTCCGTAGCTTTAAGCGGTGCCAACTGCTTAA 2626
2393 GTGATTTAGAAATCAGTAAGGCTGGAAAGAACCAACAGATCAATTAAGTCCAACTGTGAGCC 2452
2627 GTGATTTAGAAATCAGTAAGGCTGGAAAGAACCAACAGATCAATTAAGTCCAACTGTGAGCC 2686
2453 CCATCCCCACGGCCCACTGTCACTCAGTGCCACATCCACGATTTCTTGAACATCTCC 2512
2687 CCATCCCCACGGCCCACTGTCACTCAGTGCCACATCCACGATTTCTTGAACATCTCC 2746
2513 AGGACAGTGACTCCACCCCGTCAACAGCTGTGCTTTCAGAGCAGGCGAGGTGACAGTCTCA 2572
2747 AGGACAGTGACTCCACCCCGTCAACAGCTGTGCTTTCAGAGCAGGCGAGGTGACAGTCTCA 2806
2573 GTGCAGTTGCATCTCTCTCAAGAGCTTAAACAGTGCAAGTTTAAACAAACGAGCTGATTTGTT 2632
2807 GTGCCAGTTGCATCTCTCTCAAGAGCTTAAACAGTGCAAGTTTAAACAAACGAGCTGATTTGTT 2866
2633 GATGTGTTGCTGAATCAGTACGTTGAGATGTCACTAAACCTTTTGGAGATTAATTTTCAG 2692
2867 GATGTGTTGCTGAATCAGTACGTTGAGATGTCACTAAACCTTTTGGAGATTAATTTTCAG 2926
2693 GATGGAACATCTTAAACCTGAAACAGCCTTTGATTTGGGCTGGCATTTGCGAAT 2752
2927 GATGGAACATCTTAAACCTGAAACAGCCTTTGATTTGGGCTGGCATTTGCGAAT 2986
2753 TTGCAGGAAAGATTTGTTGGGAAACAGATGAATGGAATTTCCACAAACAGAAATTAAC 2812
2987 TTGCAGGAAAGATTTGTTGGGAAACAGATGAATGGAATTTCCACAAACAGAAATTAAC 3046
2813 ACTTACACAGTTTGAGTCTGGTCTTCTGTCGATATTTCTTGAAGATCTCATCTCTCC 2872
3047 ACTTACACAGTTTGAGTCTGGTCTTCTGTCGATATTTCTTGAAGATCTCATCTCTCC 3106
2873 CTGCTCTTTGACACAGTCTGCTGACAGAGGTGAGGATCATCAGGGTCAAGCATCTCTCAG 2932
3107 CTGCTCTTTGACACAGTCTGCTGACAGAGGTGAGGATCATCAGGGTCAAGCATCTCTCAG 3166
2933 CATCTAGGGATGTGCATCTATGTGATGGTGACACTTTTAGAGAACTGCTTTTGAATCCCCA 2992
3167 CATCTAGGGATGTGCATCTATGTGATGGTGACACTTTTAGAGAACTGCTTTTGAATCCCCA 3226
2993 GGGCTTTCCCTCTCTTCCATGACGGGCTCACTATCAGCCCTGAAAGTCCAACTTTCTGAA 3052
3227 GGGCTTTCCCTCTCTTCCATGACGGGCTCACTATCAGCCCTGAAAGTCCAACTTTCTGAA 3286
3053 CTTCACACAGCTGCTGCTCTGTGAGGCTGTTCCATAGAGGCCACAGGGACTGTAGCCAG 3112
3287 CTTCACACAGCTGCTGCTCTGTGAGGCTGTTCCATAGAGGCCACAGGGACTGTAGCCAG 3346
3113 GCATGACCTTTTCCAGCCGCTGCTCTGAATCCAGCACTGTGGTGGGAGGCACTCTGG 3172
3347 GCATGACCTTTTCCAGCCGCTGCTGAAATCCAGCACTGTGGTGGGAGGCACTCTGG 3406
3173 TCCTGGGGTGTGAGTGAGCCAGGGAACAAGCT----- 3206
3407 TCCTGGGGTGTGAGTGAGCCAGGGAACAAGCTTATCGATACCGTCCGAGGGGG 3466
3207 -----CAGCTTTGTTCCCTTTAGTGAGGGTTAATTTGAGCTTTGGCGTAATCA 3255
3467 GGCCCGGTACCCAGCTTTGTTCCCTTTAGTGAGGGTTAATTTGAGCTTTGGCGTAATCA 3526
3256 TGGTATAGCTGTTTCTCTGTGAAATTTGTTATCCGCTCAAAATCCACAAACATACGA 3315
3527 TGGTATAGCTGTTTCTCTGTGAAATTTGTTATCCGCTCAAAATCCACAAACATACGA 3586

3316 GCGGAAGCATAAAGTGTAAAGCCTCGGGTGCCTAATGAGTGAGCTAACTCACATTAATT 3375
3587 GCGGAAGCATAAAGTGTAAAGCCTCGGGTGCCTAATGAGTGAGCTAACTCACATTAATT 3646
3376 GCGTTGCGCTCACTGCCCCGTTTCCAGTCGGGAAACCTGTCGTGCGAGCTGCAATTAATGA 3435
3647 GCGTTGCGCTCACTGCCCCGTTTCCAGTCGGGAAACCTGTCGTGCGAGCTGCAATTAATGA 3706
3436 ATCGGCCAAGCGCGGGAGAGCGGTTTGGGTAATTTGGGGCTCTTCCGCTTCTCGCTC 3495
3707 ATCGGCCAAGCGCGGGAGAGCGGTTTGGGTAATTTGGGGCTCTTCCGCTTCTCGCTC 3766
3496 ACTGACTCGCTGCGCTCGGTCGCTGCGCGAGCGGTATCAGCTCACTCAAAAGCG 3555
3767 ACTGACTCGCTGCGCTCGGTCGCTGCGCGAGCGGTATCAGCTCACTCAAAAGCG 3826
3556 GTAATACGTTTATCCACAGATCAGGGGATAACGAGGAAAGAAACATGTGAGCAAAAGGC 3615
3827 GTAATACGTTTATCCACAGATCAGGGGATAACGAGGAAAGAAACATGTGAGCAAAAGGC 3886
3616 CAGCAAAAGCCAGGAACCGTAAAGGCGCGTTGCTGGCGTTTTTCCATAGCTCCGC 3675
3887 CAGCAAAAGCCAGGAACCGTAAAGGCGCGTTGCTGGCGTTTTTCCATAGCTCCGC 3946
3676 CCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGA 3735
3947 CCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGA 4006
3736 CTATAAGATACACAGCGGTTTCCCTCGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACC 3795
4007 CTATAAGATACACAGCGGTTTCCCTCGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACC 4066
3796 CTGCGGTTACCGGATACCTGTCCGCTTCTCCTTCCGGAAGCGTGGCGTTTCTCAT 3855
4067 CTGCGGTTACCGGATACCTGTCCGCTTCTCCTTCCGGAAGCGTGGCGTTTCTCAT 4126
3856 AGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTCGCTCCAAGCTGGGCTGTGTG 3915
4127 AGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTCGCTCCAAGCTGGGCTGTGTG 4186
3916 CACGAAACCCCGCTTTCAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAAGTCC 3975
4187 CACGAAACCCCGCTTTCAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAAGTCC 4246
3976 AACCCGTTAAGACACGACTTATCGCCACTGCGGACGCACTGGTAAACAGATTAAGCAGA 4035
4247 AACCCGTTAAGACACGACTTATCGCCACTGCGGACGCACTGGTAAACAGATTAAGCAGA 4306
4036 GCGAGGTATCTAGCGGTGCTACAGAGTTCTTGAAGTGTGGCTAACTACGGCTACACT 4095
4307 GCGAGGTATCTAGCGGTGCTACAGAGTTCTTGAAGTGTGGCTAACTACGGCTACACT 4366
4096 AGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCAGTTACCTTCGAAAAAGAGTT 4155
4367 AGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCAGTTACCTTCGAAAAAGAGTT 4426
4156 GGTAGCTCTTGATTCGGCAAAACAAACCCGCTGTTAGCGGTGGTTTTTTTGTTCGAA 4215
4427 GGTAGCTCTTGATTCGGCAAAACAAACCCGCTGTTAGCGGTGGTTTTTTTGTTCGAA 4486
4216 CAGCAGATTACGCGCAAAAAAGGATCTCAAGAGATCTTGTGATCTTTTCTACGGGG 4275
4487 CAGCAGATTACGCGCAAAAAAGGATCTCAAGAGATCTTGTGATCTTTTCTACGGGG 4546
4276 TCTGACGCTCAGAAAGTCTCGTCAAGAAAGCGATAGAAAGCGATGCGCTCGAATCGGGA 4335
4547 TCTGACGCTCAGAAAGTCTCGTCAAGAAAGCGATAGAAAGCGATGCGCTCGAATCGGGA 4606
4336 GCGCGATACCGTAAAGCAGAGAGCGGTGAGCCCATTTCCGCGCCAAAGCTCTTCAGCA 4395
4607 GCGCGATACCGTAAAGCAGAGAGCGGTGAGCCCATTTCCGCGCCAAAGCTCTTCAGCA 4666

QY 4396 ATATACGGGTAGCCAAACGCTATGTCTCTGATAGCGGTCCGCCACACCCAGCCGGCCACAG 4455
DB |||||
QY 4667 ATATACGGGTAGCCAAACGCTATGTCTCTGATAGCGGTCCGCCACACCCAGCCGGCCACAG 4726
DB |||||
QY 4456 TCGATGAATCCAGAAAGCGGCATTTTCCACCATGATATTCGGCAGCAGGATCGCCA 4515
DB |||||
QY 4727 TCGATGAATCCAGAAAGCGGCATTTTCCACCATGATATTCGGCAGCAGGATCGCCA 4786
DB |||||
QY 4516 TGGGTCAACGAGATCTCTCGCGTGGGGCATCGCGCCCTTGAGCCTTGGCGAACAGTTGG 4575
DB |||||
QY 4787 TGGGTCAACGAGATCTCTCGCGTGGGGCATCGCGCCCTTGAGCCTTGGCGAACAGTTGG 4846
DB |||||
QY 4576 GCTGGCGCAGCCCTGATGCTCTTCTGTCAGATCATCTCTGATCGACAGACCGGCTTCC 4635
DB |||||
QY 4847 GCTGGCGCAGCCCTGATGCTCTTCTGTCAGATCATCTCTGATCGACAGACCGGCTTCC 4906
DB |||||
QY 4636 ATCCGAGTACGCTCGCTCGATCGCATGTTTCTGCTTGGTGGTCCGATGGGCGAGGTAGCC 4695
DB |||||
QY 4907 ATCCGAGTACGCTCGCTCGATCGCATGTTTCTGCTTGGTGGTCCGATGGGCGAGGTAGCC 4966
DB |||||
QY 4696 GGATCAAGCGTATGACGCGCCCGCATTTGATCAGCCATGATGATGATCTTTCTCGCGAGGA 4755
DB |||||
QY 4967 GGATCAAGCGTATGACGCGCCCGCATTTGATCAGCCATGATGATGATCTTTCTCGCGAGGA 5026
DB |||||
QY 4756 GCAAGGTGATGACAGGAGATCTTGGCCCGCGCATCTTGGCCCAATAGCAGCCAGTCCCTT 4815
DB |||||
QY 5027 GCAAGGTGATGACAGGAGATCTTGGCCCGCGCATCTTGGCCCAATAGCAGCCAGTCCCTT 5086
DB |||||
QY 4816 CCGCTTCAGTGACACGTCGACGACAGCTGGCAGGAGACGCCCTGCTGGCAGCCAC 4875
DB |||||
QY 5087 CCGCTTCAGTGACACGTCGACGACAGCTGGCAGGAGACGCCCTGCTGGCAGCCAC 5146
DB |||||
QY 4876 GATAGCGCGCTCGCTCGCTCGATTCATTCAGGCGCACCGGACAGGTGCGTCTTGACA 4935
DB |||||
QY 5147 GATAGCGCGCTCGCTCGCTCGATTCATTCAGGCGCACCGGACAGGTGCGTCTTGACA 5206
DB |||||
QY 4936 AAAAGAACCGGCGCCCTCGCTGCTGACGCGGAAACACGCGGCATCAGACGACGCGATT 4995
DB |||||
QY 5207 AAAAGAACCGGCGCCCTCGCTGCTGACGCGGAAACACGCGGCATCAGACGACGCGATT 5266
DB |||||
QY 4996 GTCTGTGTGCCAGTCATAGCCGATAGCTTCTCACCAGCGCGCGGAGACCTGCG 5055
DB |||||
QY 5267 GTCTGTGTGCCAGTCATAGCCGATAGCTTCTCACCAGCGCGCGGAGACCTGCG 5326
DB |||||
QY 5056 TGCATATCCATCTGTTCAATCATGCGAAACGATCTCTCTCTCTGATCAGATCTT 5115
DB |||||
QY 5327 TGCATATCCATCTGTTCAATCATGCGAAACGATCTCTCTCTCTGATCAGATCTT 5386
DB |||||
QY 5116 GATCCCTCGCCCATCAGATCTCTTGGCGCAAGAAAGCCATCCAGTTTACTTTGCAAGGCG 5175
DB |||||
QY 5387 GATCCCTCGCCCATCAGATCTCTTGGCGCAAGAAAGCCATCCAGTTTACTTTGCAAGGCG 5446
DB |||||
QY 5176 TTCCCAACCTTACAGAGGCGGCCAGCTGGCAATTCGGTTGCTGCTGTGTCATATAA 5235
DB |||||
QY 5447 TTCCCAACCTTACAGAGGCGGCCAGCTGGCAATTCGGTTGCTGCTGTGTCATATAA 5506
DB |||||
QY 5236 ACCGCCAGCTAGCAACTGTTGGGAAGGCGCATGCTGCGGCGCTCTTCTGCTATTACGC 5295
DB |||||
QY 5507 ACCGCCAGCTAGCAACTGTTGGGAAGGCGCATGCTGCGGCGCTCTTCTGCTATTACGC 5566
DB |||||
QY 5296 CAGCTGGCGAAAGGGGATGTGTCGAAGCGCATTAAGTTGGGTACGCCAGGCTTTTCC 5355
DB |||||
QY 5567 CAGCTGGCGAAAGGGGATGTGTCGAAGCGCATTAAGTTGGGTACGCCAGGCTTTTCC 5626
DB |||||
QY 5356 CAGTACGACGTTGTAATAACGAGCGCATGTGAATTTGTAATACACTCATATAGGCGGAA 5415
DB |||||
QY 5627 CAGTACGACGTTGTAATAACGAGCGCATGTGAATTTGTAATACACTCATATAGGCGGAA 5686
DB |||||
QY 5416 TTGGAGCT 5423
DB |||||
QY 5687 TTGGAGCT 5694
DB |||||

RESULT 3

AX88054
ID AAX88054 standard; DNA; 6345 BP.
XX
AC AAX88054;
XX
XX 08-SEP-1999 (first entry)
DT
XX Plasmid pIG0100A DNA.
DE
XX
XX Plasmid pIG0100A; plasmid pIG0335; expression vector; treatment; disease;
KW RNA stability element; gene therapy; muscle atrophy; neurological;
KW muscular disease; systemic disease; aging; trophic factor; haemophilia;
KW clotting factor; atherogenesis; atherosclerotic; cardiovascular;
KW cerebrovascular; peripheral-vascular disease; hormone deficiency;
KW diabetes; transgenic animal; carcinogen; regulatory element;
KW livestock improvement; immune response; ds.
XX
OS Synthetic.
XX
XX US525564-A.
PN
XX 20-JUL-1999.
PD
XX
XX 07-JUN-1995; 95US-00472809.
PF
XX 06-NOV-1991; 91US-00789919.
PR
XX 09-MAR-1994; 94US-00209846.
PR
XX (BAYU) BAYLOR COLLEGE MEDICINE.
PA
XX
XX O'malley BW, Demayo FJ, Schwartz RJ;
PI
XX WPI; 1999-418276/35.
DR
XX
XX New expression vector system useful for gene therapy.
PT
XX
XX Disclosure; Fig 15-15G; 67pp; English.
PS
XX
XX This invention describes novel expression vector systems containing RNA
CC stability elements from 3' flanking sequences used for establishing
CC expression of a nucleic acid sequence within a tissue. The vectors also
CC facilitate enhanced expression in tissues and target expression with
CC tissue specificity. The expression vectors can be used to treat diseases
CC through gene therapy by targeting the vector to specific tissues.
CC Diseases that can be treated include muscle atrophy associated with
CC neurological, muscular or systemic disease, aging by causing tissues to
CC express trophic factors, haemophilia by causing tissues to express and
CC secrete clotting factor into the circulation, atherogenesis and
CC atherosclerotic cardiovascular, cerebrovascular or peripheral-vascular
CC disease by causing tissues to express factors involved in tissue
CC metabolism. They can be used to replace genes of inherited genetic
CC defects or acquired hormone deficiencies e.g. diabetes. To transform
CC cells to produce particular proteins or RNA in vitro. To create
CC transgenic animals which can be used for research into human diseases,
CC assessing novel therapeutic methods, assessing the effect of chemical and
CC physical carcinogens and for studying the effect of genes and genetic
CC regulatory elements or livestock improvement. They can be used to induce
CC an immune response. These vectors provide controlled expression of the
CC genes they carry and produce a significantly high level of expression.
CC Using 3'UTR sequences reduces the decay rates of the mRNAs encoded by the
CC vectors which causes increased expression
XX
SQ Sequence 6345 BP; 1453 A; 1702 C; 1689 G; 1501 T; 0 U; 0 Other;

Query Match 51.4%; Score 2785.8; DB 2; Length 6345;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2787; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 413 CCATGGGAAAAATCAGCAGCTCTTCCAAACCCCAATATTATTAAGTCGCTCTTTGATTCT 472

DB 3556 CCATGGGAAAAATCAGCAGCTCTTCCAAACCCCAATATTATTAAGTCGCTCTTTGATTCT 3615

QY	473	TGAAGGTGAAGATGCACACATGTCTCTCGCATCTCTTACCTGGGGCTGTGCTGC	532
Db	3616	TGAAGGTGAAGATGCACACATGTCTCTCGCATCTCTTACCTGGGGCTGTGCTGC	3675
QY	533	TCACTTTCACAGCTCTGCCACGGCTGGACCGGAGACGCTCTCGGGGCTGAGCTGGTG	592
Db	3676	TCACTTTCACAGCTCTGCCACGGCTGGACCGGAGACGCTCTCGGGGCTGAGCTGGTG	3735
QY	593	ATGCTCTTCAGTTCGTGTGGAGACAGGGGCTTTTATTTCACACAGCCACAGGGTATG	652
Db	3736	ATGCTCTTCAGTTCGTGTGGAGACAGGGGCTTTTATTTCACACAGCCACAGGGTATG	3795
QY	653	GCTCCAGCAGTCGGAGGGCCCTCAGACAGGTATCGTGATGATGCTGCTCCGAGCT	712
Db	3796	GCTCCAGCAGTCGGAGGGCCCTCAGACAGGTATCGTGATGATGCTGCTCCGAGCT	3855
QY	713	GTGATCTTAAGGAGGCTGGAGATGTATTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCT	772
Db	3856	GTGATCTTAAGGAGGCTGGAGATGTATTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCT	3915
QY	773	CTGTCGTGCCAGCGCCACACCGACATGCCCCAAGACCCCAAGAGGAGTACATTTGAAGA	832
Db	3916	CTGTCGTGCCAGCGCCACACCGACATGCCCCAAGACCCCAAGAGGAGTACATTTGAAGA	3975
QY	833	ACGCAAGTAGAGGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGACCTCCTGAGG	892
Db	3976	ACGCAAGTAGAGGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGACCTCCTGAGG	4035
QY	893	AGTGAAGAGTGACATGCCACCGCAGGATCCCCGGGCTGCAGGAATTCGATGGCCCCATCC	952
Db	4036	AGTGAAGAGTGACATGCCACCGCAGGATCCCCGGGCTGCAGGAATTCGATGGCCCCATCC	4095
QY	953	ATTGTCCACCGTAAATGCTTTAAACATGTTTACATGATCACTTTGCGCAACCACTCAG	1012
Db	4096	ATTGTCCACCGTAAATGCTTTAAACATGTTTACATGATCACTTTGCGCAACCACTCAG	4155
QY	1013	GATGACAACTCTGTAGGTTCCAGGCTGCTCAGGACCTCCACCGCCATGCACTTTCTAT	1072
Db	4156	GATGACAACTCTGTAGGTTCCAGGCTGCTCAGGACCTCCACCGCCATGCACTTTCTAT	4215
QY	1073	TTTGTAACAATTTCTGGTTACTGTGTGCAAAAGCTCCATGTGACACAGTGTATGTAAAG	1132
Db	4216	TTTGTAACAATTTCTGGTTACTGTGTGCAAAAGCTCCATGTGACACAGTGTATGTAAAG	4275
QY	1133	TGTACATAAATTAATTTATTTTACCTCGTTTGTGTTTTTAAACCAATGCGCTGTGG	1192
Db	4276	TGTACATAAATTAATTTATTTTACCTCGTTTGTGTTTTTAAACCAATGCGCTGTGG	4335
QY	1193	AAGGAACATAAATTTCAAGAGCATTAATCATCATGTCATTCGTGCACACCCCTAATG	1252
Db	4336	AAGGAACATAAATTTCAAGAGCATTAATCATCATGTCATTCGTGCACACCCCTAATG	4395
QY	1253	CAGTGTGTTCTGTCATCATTTTCCCTGGGCTCTTCCATCTCTCGCTGACCTGGGACTGGGT	1312
Db	4396	CAGTGTGTTCTGTCATCATTTTCCCTGGGCTCTTCCATCTCTCGCTGACCTGGGACTGGGT	4455
QY	1313	GCTGGGGCTGGGAGCAGGGTGTGGGCTCTCCAGGAGAGATGTCATGGGAGAGTGAATG	1372
Db	4456	GCTGGGGCTGGGAGCAGGGTGTGGGCTCTCCAGGAGAGATGTCATGGGAGAGTGAATG	4515
QY	1373	GGATACCTGTGGGGGGGGGAGCTCACCGCTGCTGTGGGCTGCAGGAAGCCCATTTGTGCA	1432
Db	4516	GGATACCTGTGTGGGGGGGGGAGCTCACCGCTGCTGTGGGCTGCAGGAAGCCCATTTGTGCA	4575
QY	1433	GAGAGCAGCTGGGATGCCATGACACGGGACCCCATGTCACCGTGTGTTCTCCCATGCCC	1492
Db	4576	GAGAGCAGCTGGGATGCCATGACACGGGACCCCATGTCACCGTGTGTTCTCCCATGCCC	4635
QY	1493	AGTAGGAAAGGGTTACGAGCGCGTTTCACTTCAGCTGTGAAAGGATTTTGTGGGCTC	1552
Db	4636	AGTAGGAAAGGGTTACGAGCGCGTTTCACTTCAGCTGTGAAAGGATTTTGTGGGCTC	4695
QY	1553	AGCCTGCCAGAGCAGTAGCAGGCGCATGCTGTGAGCTCCGAGCTGTGATGGACAGAGGC	1612

Db	4696	AGCCTGCCAGAGCAGTAGCAGGATGCTGTGAGCTCCGAGCTGTGATGGACAGAGGC	4755
QY	1613	AAGGCTGCAGCTGAGCCAGAGTGGTGGGCACAGTTAAATTAAGAGCTTTCCACTCCACT	1672
Db	4756	AAGGCTGCAGCTGAGCCAGAGTGGTGGGCACAGTTAAATTAAGAGCTTTCCACTCCACT	4815
QY	1673	TATGGAAGCCCTCTCGCTGCTACCTACCCCTGCTGGGGCTGGGGGCAGCCAGGGCCACTTC	1732
Db	4816	TATGGAAGCCCTCTCGCTGCTACCTACCCCTGCTGGGGCTGGGGGCAGCCAGGGCCACTTC	4875
QY	1733	CTCACCCACCTGACACACAAAGCTTTGCTGTCACACAGGACCTCTCTGTGGCCACAGA	1792
Db	4876	CTCACCCACCTGACACACAAAGCTTTGCTGTCACACAGGACCTCTCTGTGGCCACAGA	4935
QY	1793	CTCTTATAGATTGCTGTGCTTAGAGACAGGGGCTTTCCCTGCTGGCTTCTGCGC	1852
Db	4936	CTCTTATAGATTGCTGTGCTTAGAGACAGGGGCTTTCCCTGCTGGCTTCTGCGC	4995
QY	1853	CCGGGCGACACTGCAGAGCTGCCCTATCTGCTCTCTCTAGATGGTCTCTGGCAGGAAG	1912
Db	4996	CCGGGCGACACTGCAGAGCTGCCCTATCTGCTCTCTCTAGATGGTCTCTGGCAGGAAG	5055
QY	1913	CTGCACCTTGGCTTTGGGGCTGATCCATATTACCACTGCGAGTAGGACAGCACTGCTGGAAG	1972
Db	5056	CTGCACCTTGGCTTTGGGGCTGATCCATATTACCACTGCGAGTAGGACAGCACTGCTGGAAG	5115
QY	1973	AAAAGATGATTTTCAACTGAACTACTATCCAGGAGGTTATTGCTTTATTGTGATGGTG	2032
Db	5116	AAAAGATGATTTTCAACTGAACTACTATCCAGGAGGTTATTGCTTTATTGTGATGGTG	5175
QY	2033	CTAAGAGTGGTCTTTCTCACGTGAATGATTTTGGCCCTCATGTGTGAATACACTTTCCA	2092
Db	5176	CTAAGAGTGGTCTTTCTCACGTGAATGATTTTGGCCCTCATGTGTGAATACACTTTCCA	5235
QY	2093	ATAACAGCACAGCCTCCAAAGGGAAATTTCTGCAGGAAGACAGTACCTGGTGTGGAAG	2152
Db	5236	ATAACAGCACAGCCTCCAAAGGGAAATTTCTGCAGGAAGACAGTACCTGGTGTGGAAG	5295
QY	2153	TCCCTGTGAGCCCTATGTGCTTCAAGCTGAATGGCTGGGACTGGCTGGGAGACAGAT	2212
Db	5296	TCCCTGTGAGCCCTATGTGCTTCAAGCTGAATGGCTGGGACTGGCTGGGAGACAGAT	5355
QY	2213	CACATCCTTTCTTAAAGAACAAACAGAGGTAGTGTGACCTTGTGTTATTACTATT	2272
Db	5356	CACATCCTTTCTTAAAGAACAAACAGAGGTAGTGTGACCTTGTGTTATTACTATT	5415
QY	2273	TACGCGTGTGTGTTTCAAGTGGCACATACCTCAAAGGGGATATGGAGAGCTATTTCCCAAC	2332
Db	5416	TACGCGTGTGTGTTTCAAGTGGCACATACCTCAAAGGGGATATGGAGAGCTATTTCCCAAC	5475
QY	2333	CCTGCTGTGGACCCCTGATCTGGGGTTTTCTGTAGCTTAAGCGGTGCCAATGCTTAA	2392
Db	5476	CCTGCTGTGGACCCCTGATCTGGGGTTTTCTGTAGCTTAAGCGGTGCCAATGCTTAA	5535
QY	2393	GTGATTTGTAGAAATCAGTTAAGCTGGAAAGAACCAACAGATCATTAAGTCCAACTGTAGCC	2452
Db	5536	GTGATTTGTAGAAATCAGTTAAGCTGGAAAGAACCAACAGATCATTAAGTCCAACTGTAGCC	5595
QY	2453	CCATCCCGACCGGCCCACTGTCACTCAGTGCCACATCCAGGCATTTCTTGAACATCTCC	2512
Db	5596	CCATCCCGACCGGCCCACTGTCACTCAGTGCCACATCCAGGCATTTCTTGAACATCTCC	5655
QY	2513	AGGACAGTGAATCCACCCGTCACAGCTGTGCTTACAGAGCAGGAGGTGACAGTCTCA	2572
Db	5656	AGGACAGTGAATCCACCCGTCACAGCTGTGCTTACAGAGCAGGAGGTGACAGTCTCA	5715
QY	2573	GTGCCAGTTGCATCCTGCTGAGAGCTTAAACAGTGACAGTTTAAACAGGACTGATTTGTT	2632
Db	5716	GTGCCAGTTGCATCCTGCTGAGAGCTTAAACAGTGACAGTTTAAACAGGACTGATTTGTT	5775
QY	2633	GATGTGCTGTGAATCAGTACGTTGAGATGTCACTAAACCTTTTGTGGAGATTAATTTCCAG	2692

Db 5776 GATGTGTTGCTGATCAGTACGTTGAGATGTCATTAACCTTTTGGAGATTAATTTTCAG 5835
QY 2693 GATGGAACACATCTTTAAACCTGAAACAGCCTTTGATTTGGCTGGCAATTTGCGAAT 2752
Db 5836 GATGGAACACATCTTTAAACCTGAAACAGCCTTTGATTTGGCTGGCAATTTGCGAAT 5895
QY 2753 TTGACGGAAGATTTGTTGGGAACAGATGAATGAATTTCCACCAACAGAAATTAAC 2812
Db 5896 TTGACGGAAGATTTGTTGGGAACAGATGAATGAATTTCCACCAACAGAAATTAAC 5955
QY 2813 ACTTACACCAAGTTGAGTCTGCTCTCGTTGATATTTCTTAAGAATCTCATCTCTCC 2872
Db 5956 ACTTACACCAAGTTGAGTCTGCTCTCGTTGATATTTCTTAAGAATCTCATCTCTCC 6015
QY 2873 CTGCTCTTGACCAAGTCTCTGACAGGAGTGGAGATCATCAGGTCAGATCTCTCAG 2932
Db 6016 CTGCTCTTGACCAAGTCTCTGACAGGAGTGGAGATCATCAGGTCAGATCTCTCAG 6075
QY 2933 CATCTAGGAGTGCATATGTTGATGTTGACACTTTAGAGAACTGCTTTGATTCCTCA 2992
Db 6076 CATCTAGGAGTGCATATGTTGATGTTGACACTTTAGAGAACTGCTTTGATTCCTCA 6135
QY 2993 GGCCTTTCCCTCTCTTCCATGACAGGCTCACTATCAGCCCTGAAAGTCCAACTTCTGAA 3052
Db 6136 GGCCTTTCCCTCTCTTCCATGACAGGCTCACTATCAGCCCTGAAAGTCCAACTTCTGAA 6195
QY 3053 CTTCCAGCACCGTCTGCTCTGCTAGGCTCTTCCATAGAGCCACAGGAGTCTAGCCAG 3112
Db 6196 CTTCCAGCACCGTCTGCTCTGCTAGGCTCTTCCATAGAGCCACAGGAGTCTAGCCAG 6255
QY 3113 GCATGACCTTTTCCAGCCGTCTCTGAAATCCAGCACTGCTGCTGGAGGCACTCTGG 3172
Db 6256 GCATGACCTTTTCCAGCCGTCTCTGAAATCCAGCACTGCTGCTGGAGGCACTCTGG 6315
QY 3173 TCCCTGGGTGCTCAGTGCACCGAGGGAACA 3202
Db 6316 TCCCTGGGTGCTCAGTGCACCGAGGGAACA 6345

RESULT 4

AD573977
ID AD573977 standard; DNA; 2237 BP.
XX AC
XX AD573977;
XX
XX
XX 16-DEC-2004 (first entry)
XX
XX Skeletal alpha-actin 3'-end nucleotide fragment.
XX IGF-I; insulin-like growth factor I; myogenic promoter; MEF-1; MEF-2;
XX TEF-1; SRE; SP; alpha actin; growth hormone; angiogenesis; myogenesis;
XX vascular endothelial growth factor; VEGF; VEGF receptor; antidiabetic;
XX cardiac; vasotropic; ophthalmological; cerebroprotective; ds.
XX Synthetic.
XX WO2004081040-A2.
XX
XX
XX 23-SEP-2004.
XX
XX 11-MAR-2004; 2004WO-US0007295.
XX
XX 12-MAR-2003; 2003US-0454079P.
XX
XX (ADVI-) ADVISYS INC.
XX (BAYU) BAYLOR COLLEGE MEDICINE.
XX Rabinovsky ED, Draghia-Akli R;
XX WPI; 2004-668935/65.
XX
XX New isolated nucleic acid expression construct having a myogenic
PT promoter, a nucleic acid sequence encoding IGF-1le, and a 3'UTR, useful

for treating diabetes, ischemic heart and cerebrovascular disease.

Claim 6; SEQ ID NO 5; 104pp; English.

XX
PS
XX
CC The invention relates to an isolated nucleic acid expression construct
CC comprising a myogenic promoter, a nucleic acid sequence encoding an
CC insulin-like growth factor I (IGF-I) or its functional biological
CC equivalent, and a 3' untranslated region (3'UTR), which has in vivo
CC expression activity for the encoded IGF-I in a tissue. The myogenic
CC promoter in the isolated nucleic acid expression construct comprises a
CC transcriptional loci from a family of MEF-1, MEF-2, TEF-1, SRE or SP. The
CC 3'UTR is from a skeletal alpha actin gene or from a human growth hormone.
CC The expression construct further comprises transfection-facilitating
CC vector system that is a plasmid, a viral vector, a liposome, or a
CC cationic lipid. The isolated nucleic acid expression construct also
CC comprises a transfection-facilitating polypeptide having a charged
CC polypeptide and/or poly-L-glutamate. The construct is useful in a method
CC for stimulating angiogenesis, or stimulating myogenesis, or elevating
CC levels of an angiogenic factor, or stimulating endogenous production of
CC an angiopoietin, or treating a muscular or vascular complications of
CC diabetes in a subject. The angiogenic factor comprises a vascular
CC endothelial growth factor (VEGF) or VEGF receptor. The methods and
CC compositions of the present invention are useful for the prevention
CC and/or treatment of diseases or conditions associated with aberrant
CC expression or activity of the IGF-I, such as diabetes mellitus, ischaemic
CC heart disease, diabetic retinopathy and cerebrovascular disease. The
CC present sequence represents the nucleotide sequence of a skeletal alpha-
CC actin 3'-end fragment, a specific example of the 3'-UTR fragment used in
CC the nucleic acid expression construct of the invention.

XX
SQ Sequence 2237 BP; 514 A; 567 C; 569 G; 587 T; 0 U; 0 Other;

Query Match 41.3%; Score 2237; DB 13; Length 2237;

Best Local Similarity 100.0%; Pred. No. 1.5e-278;

Matches 2237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 934 GGAATTCGATGGCCCAATCCATTGTCACCGTAAATCTCTTAAACATGTTTACATGATCA 993
Db 1 GGAATTCGATGGCCCAATCCATTGTCACCGTAAATCTCTTAAACATGTTTACATGATCA 60
QY 994 CTTTGCCAAACCACTCAGATGACAATCTTGTAGGTTCCAGGCTGCTGAGGACCTCCAC 1053
Db 61 CTTTGCCAAACCACTCAGATGACAATCTTGTAGGTTCCAGGCTGCTGAGGACCTCCAC 120
QY 1054 CAGCCATGCAACTTTCTATTTTGTAAACAATTTCTGTTACTGTTGCTGCAAAAGTCCATG 1113
Db 121 CAGCCATGCAACTTTCTATTTTGTAAACAATTTCTGTTACTGTTGCTGCAAAAGTCCATG 180
QY 1114 TGACACAGTGTATGTAAGTGTAATAAATTAATTTTACCTCGTTTGTGTTTT 1173
Db 181 TGACACAGTGTATGTAAGTGTAATAAATTAATTTTACCTCGTTTGTGTTTT 240
QY 1174 TAAACCAATGCTGTGGAAGAAACATAAAACCTTCAAGAAGCATTAATCATCATGTC 1233
Db 241 TAAACCAATGCTGTGGAAGAAACATAAAACCTTCAAGAAGCATTAATCATCATGTC 300
QY 1234 TTCTGTGCACACCCCTAAATGACGTTGTTCTGTCAATCATTTCCCTGGGCTCTTCCATCTCT 1293
Db 301 TTCTGTGCACACCCCTAAATGACGTTGTTCTGTCAATCATTTCCCTGGGCTCTTCCATCTCT 360
QY 1294 CGCTGACCTGGGACCTGGGTGCTGGGCTGGGAGCAGGGGTTGGGGCTCTCCAGGGAGAGA 1353
Db 361 CGCTGACCTGGGACCTGGGTGCTGGGCTGGGAGCAGGGGTTGGGGCTCTCCAGGGAGAGA 420
QY 1354 TGGCATGGGGAGAGTATGGGATATCTGCTGGGGGGGGGGGACTCACCCCTGCTGTGGGCTG 1413
Db 421 TGGCATGGGGAGAGTATGGGATATCTGCTGGGGGGGGGGGACTCACCCCTGCTGTGGGCTG 480
QY 1414 CAGGAGCCCATTTGGTGCAGAGGACGCTGGGATGCCCATGACACGGGACCCACTGCA 1473
Db 481 CAGGAGCCCATTTGGTGCAGAGGACGCTGGGATGCCCATGACACGGGACCCACTGCA 540
QY 1474 CCGTGTGTTCTCCCATGCCAGTAGGAAAGGGTTACGAGCGCGGTTTCATTCTCAGCTTGT 1533

PT Treatment of urinary incontinence - by delivering nucleic acid vector for
XX expression of growth factor or neurotrophic factor in tissue(s).

PS Disclosure; Page 105-107; 117pp; English.

CC A method has been developed of treating urinary incontinence (UI) in
CC mammals. The method comprises delivering a nucleic acid vector for the
CC expression of a growth factor or neurotrophic factor in a tissue or
CC tissues. The present sequence represents the actual lower sequence of
CC plasmid pIG0552 nucleotides 1-3599 from the present invention. Due to the
CC growth and stimulatory effects of growth factors and neurotrophic
CC factors, introducing these factors to degenerated muscles in the urinary
CC system can improve UI by enhancing both their integrity and neural
CC innervation

XX Sequence 3599 BP; 733 A; 1098 C; 1042 G; 726 T; 0 U; 0 Other;

Query Match 40.9%; Score 2218; DB 2; Length 3599;
Best Local Similarity 99.6%; Pred. No. 3.7e-276; Mismatches 10; Indels 0; Gaps 0;
Matches 2224; Conservative 0;

Qy	3190	GAGCCAGGGAACAGCTCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCG	3249
Db	3	GAGGGGGGGCCGGTACCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCG	62
Qy	3250	TAATCATGTCATAGCTGTTTCTGTGTGAAATTTGTTATCCGCTCAAAATTCACACAAC	3309
Db	63	TAATCATGTCATAGCTGTTTCTGTGTGAAATTTGTTATCCGCTCAAAATTCACACAAC	122
Qy	3310	ATAGGAGCCGGAAGCATAAAGTGTAAAGCTTGGGTGCTTAATGAGTGAGCTCACTACA	3369
Db	123	ATAGGAGCCGGAAGCATAAAGTGTAAAGCTTGGGTGCTTAATGAGTGAGCTCACTACA	182
Qy	3370	TTAATTCGCTTGGCTCAGCTGCGCTTTCAGTTCGGGAACCTGCTGCGAGCTGCAT	3429
Db	183	TTAATTCGCTTGGCTCAGCTGCGCTTTCAGTTCGGGAACCTGCTGCGAGCTGCAT	242
Qy	3430	TAATGAATCGGCCAAGCGCGGGGAGGCGGTTTGGTATTTGGGCGCTTCCGCTTCC	3489
Db	243	TAATGAATCGGCCAAGCGCGGGGAGGCGGTTTGGTATTTGGGCGCTTCCGCTTCC	302
Qy	3490	TCGCTCACTGACTGCTGCGCTCGTTCGCTGCGGTGCGGAGCGGTATCAGCTCACTCA	3549
Db	303	TCGCTCACTGACTGCTGCGCTCGTTCGCTGCGGTGCGGAGCGGTATCAGCTCACTCA	362
Qy	3550	AAGCGGTATACGTTTATCCAGAAATCAGGGGATTAACGAGGAAGACATGTGAGCA	3609
Db	363	AAGCGGTATACGTTTATCCAGAAATCAGGGGATTAACGAGGAAGACATGTGAGCA	422
Qy	3610	AAAGGCCAGCAAAAGGCCAGGAACCGTAAAGGCCGCTTGTGGCGTTTTCATAGG	3669
Db	423	AAAGGCCAGCAAAAGGCCAGGAACCGTAAAGGCCGCTTGTGGCGTTTTCATAGG	482
Qy	3670	CTCGGCCCTTGAAGGATCAAAATATCGACGCTCAAGTCAGAGGTGGCGAAACCCG	3729
Db	483	CTCGGCCCTTGAAGGATCAAAATATCGACGCTCAAGTCAGAGGTGGCGAAACCCG	542
Qy	3730	ACAGGACTATAAGATACAGGCGTTTCCCTCGGAGCTCCCTCGTGGCTCTCTCTGTT	3789
Db	543	ACAGGACTATAAGATACAGGCGTTTCCCTCGGAGCTCCCTCGTGGCTCTCTCTGTT	602
Qy	3790	CCGACCTCGCGTTACCGGATACCTGTCGCGCTTCTTCCTTCCGGAAGCGTGGCGCTT	3849
Db	603	CCGACCTCGCGTTACCGGATACCTGTCGCGCTTCTTCCTTCCGGAAGCGTGGCGCTT	662
Qy	3850	TCTCATAGCTCAAGCTGTAGTATCTCAGTTCGGTGTAGTGTGCTTCGCTCAAGCTGGC	3909
Db	663	TCTCATAGCTCAAGCTGTAGTATCTCAGTTCGGTGTAGTGTGCTTCGCTCAAGCTGGC	722
Qy	3910	TGTGTGACGAAACCCCGCTTACGCGGACCGCTGCGCTTATCCGGTAACTATGCTCTT	3969
Db	723	TGTGTGACGAAACCCCGCTTACGCGGACCGCTGCGCTTATCCGGTAACTATGCTCTT	782

Qy	3970	GAGTCCAAACCCGGTAAAGACACGACTTATTCGCCACTGCGAGCAGCCTGTTAAACAGATT	4029
Db	783	GAGTCCAAACCCGGTAAAGACACGACTTATTCGCCACTGCGAGCAGCCTGTTAAACAGATT	842
Qy	4030	AGCAGAGCGAGGTATGTAGCGGTGTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC	4089
Db	843	AGCAGAGCGAGGTATGTAGCGGTGTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC	902
Qy	4090	TACACTAGAGAAACAGTATTGTTGTTATCTGCGCTCTGCTGAAGCCAGTTACTCTCGGAAA	4149
Db	903	TACACTAGAGAAACAGTATTGTTGTTATCTGCGCTCTGCTGAAGCCAGTTACTCTCGGAAA	962
Qy	4150	AGAGTTGGTAGCTTCTGATCCGCGCAAAACCAACCGCTGCTAGCGGTGTTTTTTGTT	4209
Db	963	AGAGTTGGTAGCTTCTGATCCGCGCAAAACCAACCGCTGCTAGCGGTGTTTTTTGTT	1022
Qy	4210	TGCAAGCAGCAGATTACGCGCAGAAAAGAGATCTCAAGAGATCTCTTGTATCTTTCT	4269
Db	1023	TGCAAGCAGCAGATTACGCGCAGAAAAGAGATCTCAAGAGATCTCTTGTATCTTTCT	1082
Qy	4270	ACGGGCTCTGACGCTCAGAGAACTCGTCAAGAGGCGATAGAGGCGATCGCGTCGAA	4329
Db	1083	ACGGGCTCTGACGCTCAGAGAACTCGTCAAGAGGCGATAGAGGCGATCGCGTCGAA	1142
Qy	4330	TCGGGAGCGCGATACCGTAAAGCAGAGAGCGGTTCAGCCCATTCGCCCGCAAGCTCT	4389
Db	1143	TCGGGAGCGCGATACCGTAAAGCAGAGAGCGGTTCAGCCCATTCGCCCGCAAGCTCT	1202
Qy	4390	TCAGCAATATCAGCGGTAGCAACGCTATGTCTGTATAGCGGTCCGCGCACACCCAGCGG	4449
Db	1203	TCAGCAATATCAGCGGTAGCAACGCTATGTCTGTATAGCGGTCCGCGCACACCCAGCGG	1262
Qy	4450	CCACAGTCATGAATCCAGAAAAGCGCCATTTTCCACATGATATTCGGCAAGCAGGCA	4509
Db	1263	CCACAGTCATGAATCCAGAAAAGCGCCATTTTCCACATGATATTCGGCAAGCAGGCA	1322
Qy	4510	TCGCCATGGTTCACGAGAGATCTTCGCCGTCCGGCATCGCGCTTCGAGCCTGGCGAAC	4569
Db	1323	TCGCCATGGTTCACGAGAGATCTTCGCCGTCCGGCATCGCGCTTCGAGCCTGGCGAAC	1382
Qy	4570	AGTTCCGCTGGCGAGCGCTGATGCTCTTCTGTCCAGATCATCTGTATCGAAGACCG	4629
Db	1383	AGTTCCGCTGGCGAGCGCTGATGCTCTTCTGTCCAGATCATCTGTATCGAAGACCG	1442
Qy	4630	GCTTCATCCGAGTACGTCGTCGATGCGATGTTTGGTGGTGGTGGTGGGCG	4689
Db	1443	GCTTCATCCGAGTACGTCGTCGATGCGATGTTTGGTGGTGGTGGTGGGCG	1502
Qy	4690	GTAGCCGATCAAGCGTATGCGCCCGCATTCGCATCGACCATGATGATCTTTCTCG	4749
Db	1503	GTAGCCGATCAAGCGTATGCGCCCGCATTCGCATCGACCATGATGATCTTTCTCG	1562
Qy	4750	GCAGGAGAGGTGAGATGACAGGAGATCTTGCCTCCGCGCATTCGCGCCAAATAGCAGCG	4809
Db	1563	GCAGGAGAGGTGAGATGACAGGAGATCTTGCCTCCGCGCATTCGCGCCAAATAGCAGCG	1622
Qy	4810	TCCTTCCCGCTTCAGTGACAGCTCGAGCAGAGCTCGCAAGGAAACGCCCTGCTGGCC	4869
Db	1623	TCCTTCCCGCTTCAGTGACAGCTCGAGCAGAGCTCGCAAGGAAACGCCCTGCTGGCC	1682
Qy	4870	AGCCAGATAGCGCGCTGCTCTGTCAGTTCATTTCAGGGCAGCGGACAGGTGGTC	4929
Db	1683	AGCCAGATAGCGCGCTGCTCTGTCAGTTCATTTCAGGGCAGCGGACAGGTGGTC	1742
Qy	4930	TTGACAAAAGAAACCGGGCGCCCTGCTGACAGCGCGAAACCGCGCGCATCAGAGCAG	4989
Db	1743	TTGACAAAAGAAACCGGGCGCCCTGCTGACAGCGCGAAACCGCGCGCATCAGAGCAG	1802
Qy	4990	CCGATGCTGTTGTCGCCAGTCATAGCCGATAGCTCTCCACCCAAAGCGCGGAGAA	5049
Db	1803	CCGATGCTGTTGTCGCCAGTCATAGCCGATAGCTCTCCACCCAAAGCGCGGAGAA	1862
Qy	5050	CCTGCGTCAATCCATCTTTGTTCAATCATGCGAAACGATCTCTCTCTCTCTCTCTCTCT	5109

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Db 1863 CCTGGTGCAATCATCTTGTTCATCATCGAAACGATCCTCATCTGTCTCTGTATCA 1922
Qy 5110 GATCTTGATCCCTGCGCCATCAGATCCTTGGCGGGAAGAACCCATCCAGTTACTTTG 5169
Db 1923 GATCTTGATCCCTGCGCCATCAGATCCTTGGCGGGAAGAACCCATCCAGTTACTTTG 1982
Qy 5170 CAGGGCTTCCCACTTACAGAGGGGCGCCAGCTGGCAATTCCGGTTTCGCTTGCCTGTC 5229
Db 1983 CAGGGCTTCCCACTTACAGAGGGGCGCCAGCTGGCAATTCCGGTTTCGCTTGCCTGTC 2042
Qy 5230 CATAAAACCCGCCAGTCTAGCACTGTGTGGGAAGGGCGATCGGTGGCGGCTCTTTCGCTA 5289
Db 2043 CATAAAACCCGCCAGTCTAGCACTGTGTGGGAAGGGCGATCGGTGGCGGCTCTTTCGCTA 2102
Qy 5290 TTACGCCAGCTGGCGAAAGGGGGATGTCTGCAAGGCGATTAAGTTGGTTAACGCCAGGG 5349
Db 2103 TTACGCCAGCTGGCGAAAGGGGGATGTCTGCAAGGCGATTAAGTTGGTTAACGCCAGGG 2162
Qy 5350 TTTTCCAGTCACGACGTTGTAAAACGACGCCAGTCAATTTGTAATACGACTCACTATAG 5409
Db 2163 TTTTCCAGTCACGACGTTGTAAAACGACGCCAGTCAATTTGTAATACGACTCACTATAG 2222
Qy 5410 GCGCAATTGGAGCT 5423
Db 2223 GCGCAATTGGAGCT 2236

RESULT 6
AAV40796
ID AAV40796 standard; DNA; 3599 BP.
AC AAV40796;
XX
XX
XX 23-SEP-1998 (first entry)
XX
XX Actual sequence of IGF-I containing plasmid pIG0552.
XX
XX IGF-I; insulin-like growth factor I; skeletal alpha-actin gene promoter;
XX muscle atrophy; diabetes; osteoporosis; growth disorder; therapy; AIDS;
XX Chacot-marie-tooth disease; atherogenesis; haemophilia; neuropathy; ss.
XX
XX Synthetic.
XX
XX WO9824922-A1.
XX
XX 11-JUN-1998.
XX
XX 01-DEC-1997; 97WO-US021852.
XX
XX 02-DEC-1996; 96US-0031539P.
XX
XX 19-NOV-1997; 97US-00974572.
XX
XX (GENE-) GENEMEDICINE INC.
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
XX Coleman M, Schwartz R, Demayo FJ;
XX
XX WPI; 1998-333339/29.
XX
XX New vector for expression of insulin-like growth factor-I - containing a
XX skeletal alpha-actin gene promoter, IGF-I coding sequences and a 3'
XX region from growth hormone 3'-UTR.
XX
XX Claim 16; Page 37-41; 115pp; English.
XX
XX This sequence is the actual sequence for pIG0552 which is an example of a
XX vector of the invention. The vector is for expression of a nucleic acid
XX sequence in a cell, and comprises: (a) a nucleic acid cassette containing
XX a sequence encoding insulin-like growth factor-I (IGF-I); (b) a 5'
XX flanking region including one or more sequences necessary for expression
XX of the nucleic acid cassette, including a promoter from a skeletal alpha-
XX actin gene; (c) a linker connecting the 5' flanking region to a nucleic
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CC acid, the linker having a position for inserting the nucleic acid
CC cassette, and lacking the coding sequence of a gene with which it is
CC naturally associated; and (d) a 3' flanking region, including a 3',
CC untranslated region or a 3' non coding region or both, where the 3'
CC flanking region is 3' to the position for inserting the nucleic acid
CC cassette and comprises a sequence from a growth hormone 3'-UTR. The
CC vector can provide for efficient IGF-I expression, particularly in gene
CC therapy. It can be used for the delivery of IGF-I for treating diseases
CC such as muscle atrophy, diabetes, neuropathy, osteoporosis, and growth
CC disorders. They can be used for treating peripheral neuropathies
CC resulting from diabetes, genetic disease such as Type I or Type II
CC diabetes, genetic disease such as Chacot-marie-tooth disease, AIDS,
CC atherogenesis, atherosclerotic, cardiovascular, cerebrovascular, or
CC peripheral vascular disease, haemophilia, inflammation and side-effects
CC from anti-cancer and anti-viral drugs. The vectors can also be used to
CC create transgenic animals for research or livestock improvement
XX
XX Sequence 3599 BP; 733 A; 1098 C; 1042 G; 726 T; 0 U; 0 Other;
SQ
Query Match 40.9%; Score 2218; DB 2; Length 3599;
Best Local Similarity 99.6%; Pred. No. 3.7e-276;
Matches 2224; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 3190 GAGCCAGGGAAACAGCTCAGCTTTTGTTCCTTTAGTGGGGTTAATTCAGCTTGGCG 3249
Db 3 GAGGGGGGGCGCGTACCAGCTTTTGTTCCTTTAGTGGGGTTAATTCAGCTTGGCG 62
Qy 3250 TAATCATGTCATAGCTGTTTCTCTGTGTAATTTATCCGCTCACAATTCACACAAC 3309
Db 63 TAATCATGTCATAGCTGTTTCTCTGTGTAATTTATCCGCTCACAATTCACACAAC 122
Qy 3310 ATACGAGCCGGAAGCATAAAGTGTAAAGCTGGGGTGCCTTAATGAGTGAGCTAATCACA 3369
Db 123 ATACGAGCCGGAAGCATAAAGTGTAAAGCTGGGGTGCCTTAATGAGTGAGCTAATCACA 182
Qy 3370 TTAATTGCGTTGCGCTCACTGCCCGCTTTCAGTTCGGGAAAACCTGTCGTCAGCTGCAT 3429
Db 183 TTAATTGCGTTGCGCTCACTGCCCGCTTTCAGTTCGGGAAAACCTGTCGTCAGCTGCAT 242
Qy 3430 TAATGAATCGGCCAAGCGCGGGAGGCGGTTTGGTATTTGGCGCTCTTCGCGTTCC 3489
Db 243 TAATGAATCGGCCAAGCGCGGGAGGCGGTTTGGTATTTGGCGCTCTTCGCGTTCC 302
Qy 3490 TCGCTCACTGACTCGCTGCGCTGCGGTTCGGGTGCGGCGAGCGGTATCAGCTCACTCA 3549
Db 303 TCGCTCACTGACTCGCTGCGCTGCGGTTCGGGTGCGGCGAGCGGTATCAGCTCACTCA 362
Qy 3550 AAGCGGTAATACGGTTATCCACAGATCAGGGGATTAACGAGGAAGAATGTGAGCA 3609
Db 363 AAGCGGTAATACGGTTATCCACAGATCAGGGGATTAACGAGGAAGAATGTGAGCA 422
Qy 3610 AAAGGCCAGCAAAAGGCCAGGNAACCGTAAAGGCCCGCTTTCGCGGTTTTCATATAGG 3669
Db 423 AAAGGCCAGCAAAAGGCCAGGNAACCGTAAAGGCCCGCTTTCGCGGTTTTCATATAGG 482
Qy 3670 CTCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAAGTCAAGTGGCGGAAAACCG 3729
Db 483 CTCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAAGTGGCGGAAAACCG 542
Qy 3730 ACAGGACTATAAAGATACAGGGGTTTCCCGCTGGAAAGCTCCCTCGTGGCTCTCTGTT 3789
Db 543 ACAGGACTATAAAGATACAGGGGTTTCCCGCTGGAAAGCTCCCTCGTGGCTCTCTGTT 602
Qy 3790 CCGACCTTGGCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
Db 603 CCGACCTTGGCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGCTT 662
Qy 3850 TCTCATAGCTCACGCTTAGGTATCTCAGTTTCGGTGTAGTGTGTTTCGCTCCAAGCTGGGC 3909
Db 663 TCTCATAGCTCACGCTTAGGTATCTCAGTTTCGGTGTAGTGTGTTTCGCTCCAAGCTGGGC 722
Qy 3910 TGTGTGACGAAACCCCGCTTACGCCGACCGCTTACCGCTTATTCGGTAACTATCGTCTT 3969
Db 3910 TGTGTGACGAAACCCCGCTTACGCCGACCGCTTACCGCTTATTCGGTAACTATCGTCTT
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4990 CCAGTTGCTGTTGTCGCCAGTCATAGCCGAATAGCTCTCCACCAAGCGCGGAGAA 5049
Db CCAGTTGCTGTTGTCGCCAGTCATAGCCGAATAGCTCTCCACCAAGCGCGGAGAA 3429
QY 5050 CTTGCGTGCATCATCTTGTTCATCATGCGAAACGATCTCATCTGCTCTTGATCA 5109
Db CCTGCGTGCATCATCTTGTTCATCATGCGAAACGATCTCATCTGCTCTTGATCA 3489
QY 5110 GATCTTTGATCCCTGGCCCATCAGATCTTGGCGCAAGAAAGCCATCCAGTTTACTTTG 5169
Db GATCTTTGATCCCTGGCCCATCAGATCTTGGCGCAAGAAAGCCATCCAGTTTACTTTG 3549
QY 5170 CAGGGCTTCCCAACTTACAGAGGCGCCCGCCAGCTGGCAATTCGGTTTCGCTTGTCTC 5229
Db CAGGGCTTCCCAACTTACAGAGGCGCCCGCCAGCTGGCAATTCGGTTTCGCTTGTCTC 3609
QY 5230 CATAAACCCGCCAGCTTAGCACTGTTGGGAAGGGCGATCGGTGGGGCTCTTCGCTA 5289
Db CATAAACCCGCCAGCTTAGCACTGTTGGGAAGGGCGATCGGTGGGGCTCTTCGCTA 3669
QY 5290 TTACGCCAGCTGGCGAAGGGGATGTGCTGCAAGGCGATTAAAGTTGGGTAAGCCAGGG 5349
Db TTACGCCAGCTGGCGAAGGGGATGTGCTGCAAGGCGATTAAAGTTGGGTAAGCCAGGG 3729
QY 5350 TTTTCCAGTCACGACGTTGTAAACCGACGCGCAGTGAAATTGTAATACGACTCACTATAG 5409
Db TTTTCCAGTCACGACGTTGTAAACCGACGCGCAGTGAAATTGTAATACGACTCACTATAG 3789
QY 5410 GCGCAATTGGAGCT 5423
Db GCGCAATTGGAGCT 3803

RESULT 8

AAV50427
ID AAV50427 standard; DNA; 3600 BP.

AC AAV50427;

XX 26-OCT-1998 (first entry)

DT Plasmid pIG0552 upper expected sequence nucleotides 1-3600.

DE Human; IGF-1; insulin-like growth factor 1; urinary incontinence;

XX gene therapy; neurotrophic factor; ss.

XX Synthetic.

OS Homo sapiens.

XX W09833529-A1.

XX 06-AUG-1998.

XX 04-FEB-1998; 98WO-US002051.

XX 04-FEB-1997; 97US-0036862P.

XX (GENE-) GENEMEDICINE INC.

XX Coleman M;

XX WPI; 1998-437184/37.

XX Treatment of urinary incontinence - by delivering nucleic acid vector for
PT expression of growth factor or neurotrophic factor in tissue (s).

PS Disclosure; Page 103-105; 117pp; English.

XX A method has been developed of treating urinary incontinence (UI) in
CC mammals. The method comprises delivering a nucleic acid vector for the
CC expression of a growth factor or neurotrophic factor in a tissue or
CC tissues. The present sequence represents the expected upper sequence of

CC Plasmid pIG0552 nucleotides 1-3600 from the present invention. Due to the
CC growth and stimulating effects of growth factors and neurotrophic
CC factors, introducing these factors to degenerated muscles in the urinary
CC system can improve UI by enhancing both their integrity and neural
CC innervation

XX Sequence 3600 BP; 733 A; 1099 C; 1042 G; 726 T; 0 U; 0 Other;

QY Query Match 40.9%; Score 2215.8; DB 2; Length 3600;

Best Local Similarity 99.9%; Pred. No. 7e-276;

Matches 2217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3205 CTCAGCTTTTGTCCCTTTAGTCAGGGTTAAATTCGAGCTTGGCTTAATCATGTCTATAG 3264

Db 19 CCAGCTTTTGTCCCTTTAGTCAGGGTTAAATTCGAGCTTGGCTTAATCATGTCTATAG 78

QY 3265 CTGTTTCTCTGTGTAATTTGTTATCCGCTCACAAATTCACACAAATACGAGCGGGAAGC 3324

Db 79 CTGTTTCTCTGTGTAATTTGTTATCCGCTCACAAATTCACACAAATACGAGCGGGAAGC 138

QY 3325 ATAAAGTGTAAAGCCTTGGGCTTAATGAGTGAGCTAACTCACATTAATTTGGTGTTCGCG 3384

Db 139 ATAAAGTGTAAAGCCTTGGGCTTAATGAGTGAGCTAACTCACATTAATTTGGTGTTCGCG 198

QY 3385 TCACTGCCCGCTTTCAGTCGGGAAACCTGTCTGTCCAGCTGATTAATGAATCGGCCAA 3444

Db 199 TCACTGCCCGCTTTCAGTCGGGAAACCTGTCTGTCCAGCTGATTAATGAATCGGCCAA 258

QY 3445 CGCGCGGAGAGCGGTTTGGCTATTTGGGCGCTCTTCCGCTTCCCTCGCTCACTGACTCG 3504

Db 259 CGCGCGGAGAGCGGTTTGGCTATTTGGGCGCTCTTCCGCTTCCCTCGCTCACTGACTCG 318

QY 3505 CTGCGCTCGGTCGTTCCGCTGCGGCGAGCGGTATCAGCTCACTCAAAGCGGTAATACGG 3564

Db 319 CTGCGCTCGGTCGTTCCGCTGCGGCGAGCGGTATCAGCTCACTCAAAGCGGTAATACGG 378

QY 3565 TTATCCACAGAAATCAGGGGATTAACGAGGAAAGAAACATGTGAGCAAAGGCGAGCAAAAG 3624

Db 379 TTATCCACAGAAATCAGGGGATTAACGAGGAAAGAAACATGTGAGCAAAGGCGAGCAAAAG 438

QY 3625 GCCAGGAACGGTAAAGGCGGTTGCTGGCGGCTTTTCCATAGGCTCCGCCCCCTGAC 3684

Db 439 GCCAGGAACGGTAAAGGCGGTTGCTGGCGGCTTTTCCATAGGCTCCGCCCCCTGAC 498

QY 3685 GAGCATCACAAAATCGAGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGA 3744

Db 499 GAGCATCACAAAATCGAGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGA 558

QY 3745 TACCAGCGGTTTCCCGCTGGAAGCTCCCTCGTCGCTCTCTCTGTCGACCCCTGCGCTT 3804

Db 559 TACCAGCGGTTTCCCGCTGGAAGCTCCCTCGTCGCTCTCTCTGTCGACCCCTGCGCTT 618

QY 3805 ACCGATACCTGTCCGCTTTCCTTCCGGAAGCGTGGCGCTTCTCATAGCTACGC 3864

Db 619 ACCGATACCTGTCCGCTTTCCTTCCGGAAGCGTGGCGCTTCTCATAGCTACGC 678

QY 3865 TGTAGGTATCTCAGTTCCGCTGAGTGTGCTTCCGCTCCAAGCTGCTGTGTGACGAACCC 3924

Db 679 TGTAGGTATCTCAGTTCCGCTGAGTGTGCTTCCGCTCCAAGCTGCTGTGTGACGAACCC 738

QY 3925 CCGCTTCAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCCAAACCCGTA 3984

Db 739 CCGCTTCAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGTAGTCCAAACCCGTA 798

QY 3985 AGACAGACTTATCGGCACTGGCAGCGCCACTGGTAAAGGATTTAGCAGCGGAGGTAT 4044

Db 799 AGACAGACTTATCGGCACTGGCAGCGCCACTGGTAAAGGATTTAGCAGCGGAGGTAT 858

QY 4045 GTAGGCGGTCTACAGAGTTCTTTGAAAGTGTGCGCTAACTACGCTACACTAGAGAACA 4104

Db 859 GTAGGCGGTCTACAGAGTTCTTTGAAAGTGTGCGCTAACTACGCTACACTAGAGAACA 918

QY 4105 GTATTTGGTATCTCGCTCTGCTGAAAGCCAGTTACCTTCGGAAGAGGTGGTAGCTCT 4164

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Db 919 GTATTGTTGTAATCTGCGCTCTGCTGAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCT 978
QY 4165 TGATCCGGCAAAACAAACCCGCTGTGTAGCGGTGGTTTTTTTGTGTGCAAGCAGCAGATT 4224
Db 979 TGATCCGGCAAAACAAACCCGCTGTGTAGCGGTGGTTTTTTTGTGTGCAAGCAGCAGATT 1038
QY 4225 ACCGCGAGAAAAAGAGATCTCAAGAGATCCTTTGATCTTTTCTACGGGGTCTGACGCT 4284
Db 1039 ACCGCGAGAAAAAGAGATCTCAAGAGATCCTTTGATCTTTTCTACGGGGTCTGACGCT 1098
QY 4285 CAGAGAATCTCGTCAAGAAAGCGATAGAAAGCGATGCGCTGCGCAATCGGAGGCGGCGATA 4344
Db 1099 CAGAGAATCTCGTCAAGAAAGCGATAGAAAGCGATGCGCTGCGCAATCGGAGGCGGCGATA 1158
QY 4345 CCCTAAAGCAGAGAAAGCGGTGAGCCCATTCGCGCCCAAGCTCTTTCAGCAATATACAGG 4404
Db 1159 CCCTAAAGCAGAGAAAGCGGTGAGCCCATTCGCGCCCAAGCTCTTTCAGCAATATACAGG 1218
QY 4405 GTAGCCAAACGCTATGCTCTGATAGCGGTCCGCCACACCCAGCCGCGCCACAGTCGATGAAT 4464
Db 1219 GTAGCCAAACGCTATGCTCTGATAGCGGTCCGCCACACCCAGCCGCGCCACAGTCGATGAAT 1278
QY 4465 CCAGAAAAGCGCCCATTTTCCACCATGATATTCGGCAAGCAGGATCGCCATCGGTCAAG 4524
Db 1279 CCAGAAAAGCGCCCATTTTCCACCATGATATTCGGCAAGCAGGATCGCCATCGGTCAAG 1338
QY 4525 ACAGATGCTTCGCGGTGCGGATGCGCGCTTGAGCTGCGCAACAGTTCGGTGGCGCG 4584
Db 1339 ACAGATGCTTCGCGGTGCGGATGCGCGCTTGAGCTGCGCAACAGTTCGGTGGCGCG 1398
QY 4585 AGCCCTGATGCTCTTCGTCAGATCATCTGATCGACAGACCGGCTTCATCCGAGTA 4644
Db 1399 AGCCCTGATGCTCTTCGTCAGATCATCTGATCGACAGACCGGCTTCATCCGAGTA 1458
QY 4645 CGTCTCGCTCGATGCGATGTTTCGCTTGTGTGTCGAATGGGCAAGTAGCGGATCAAGC 4704
Db 1459 CGTCTCGCTCGATGCGATGTTTCGCTTGTGTGTCGAATGGGCAAGTAGCGGATCAAGC 1518
QY 4705 GTATGACGCGCGCATTTGATCATGAGCCATGATGATATCTTCTCGGAGGAGCAAGTGA 4764
Db 1519 GTATGACGCGCGCATTTGATCATGAGCCATGATGATATCTTCTCGGAGGAGCAAGTGA 1578
QY 4765 GATGACAGGAGATCCTTCGCGCGCACTTCGCCCAATAGCAGCCAGTCCCTTCCGCTTCA 4824
Db 1579 GATGACAGGAGATCCTTCGCGCGCACTTCGCCCAATAGCAGCCAGTCCCTTCCGCTTCA 1638
QY 4825 GTGACAAAGTCGAGCAGCAGCTGCGCAAGAAAGCGCCGCTGTCGGCCAGCCAGTAGCCGC 4884
Db 1639 GTGACAAAGTCGAGCAGCAGCTGCGCAAGAAAGCGCCGCTGTCGGCCAGCCAGTAGCCGC 1698
QY 4885 GCTGCTCTGCTCTGAGTTCATTCAGGGCACCAGCAGGTGCTGTTTGACAAAAGAAC 4944
Db 1699 GCTGCTCTGCTCTGAGTTCATTCAGGGCACCAGCAGGTGCTGTTTGACAAAAGAAC 1758
QY 4945 GGGGCCCCCTGCTGACAGCCGGAACACGCGCGCATCAGAGCAGCGATGCTGTTGT 5004
Db 1759 GGGGCCCCCTGCTGACAGCCGGAACACGCGCGCATCAGAGCAGCGATGCTGTTGT 1818
QY 5005 GCCCAGTCATAGCCGAATAGCTCTTCCACCCCAAGCGCGGAGAACCTGCGTCAATCCA 5064
Db 1819 GCCCAGTCATAGCCGAATAGCTCTTCCACCCCAAGCGCGGAGAACCTGCGTCAATCCA 1878
QY 5065 TCTTGTTCATATCGAAAGCATCTCATCTGCTCTCTTGTATCAGATCTTTGATCCCTG 5124
Db 1879 TCTTGTTCATATCGAAAGCATCTCATCTGCTCTCTTGTATCAGATCTTTGATCCCTG 1938
QY 5125 CGCATCAGATCTTGGCGGGAAGAACGCAATCAGTTTACTTTGAGGGCTTCCCAACC 5184
Db 1939 CGCATCAGATCTTGGCGGGAAGAACGCAATCAGTTTACTTTGAGGGCTTCCCAACC 1998
QY 5185 TTACACAGGGCGCCCGAGCTGGCAATTCGCGGTTGCTGTGTCCTCAATAAACCGCCAG 5244
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RESULT 9

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AAV40795
ID AAV40795 standard; DNA; 3600 BP.
XX
AC AAV40795;
XX
XX 23-SBP-1998 (first entry)
XX
DE Expected sequence of IGF-I containing plasmid pIG0552.
XX
XX IGF-I; insulin-like growth factor I; skeletal alpha-actin gene promoter;
KW muscle atrophy; diabetes; osteoporosis; growth disorder; therapy; AIDS;
KW Chacot-marie-tooth disease; atherogenesis; haemophilia; neuropathy; ss.
XX
XX Synthetic.
XX
XX WO9824922-A1.
XX
XX 11-JUN-1998.
XX
XX 01-DEC-1997; 97WO-US021852.
XX
XX 02-DEC-1996; 96US-0031539P.
XX 19-NOV-1997; 97US-00974572.
XX
XX (GENE-) GENEMEDICINE INC.
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
XX Coleman M, Schwartz R, Demayo FJ;
XX
XX WPI; 1998-333339/29.
```

New vector for expression of insulin-like growth factor-I - containing a skeletal alpha-actin gene promoter, IGF-I coding sequences and a 3' region from growth hormone 3'-UTR.

Claim 16; Page 37-41; 115pp; English.

This sequence is the expected sequence for pIG0552 which is an example of a vector of the invention. The vector is for expression of a nucleic acid sequence in a cell, and comprises: (a) a nucleic acid cassette containing a sequence encoding insulin-like growth factor-I (IGF-I); (b) a 5' flanking region including one or more sequences necessary for expression of the nucleic acid cassette, including the 5' flanking region to a skeletal alpha-actin gene; (c) a linker connecting the 5' flanking region to a nucleic acid, the linker having a position for inserting the nucleic acid cassette, and lacking the coding sequence of a gene with which it is naturally associated; and (d) a 3' flanking region, including a 3' untranslated region or a 3' non coding region or both, where the 3' flanking region is 3' to the position for inserting the nucleic acid cassette and comprises a sequence from a growth hormone 3'-UTR. The vector can provide for efficient IGF-I expression, particularly in gene therapy. It can be used for the delivery of IGF-I for treating diseases such as muscle atrophy, diabetes, neuropathy, osteoporosis, and growth disorders. They can be used for treating peripheral neuropathies resulting from diabetes, genetic disease such as Type I or Type II diabetes, genetic disease such as Chacot-marie-tooth disease, AIDS, atherogenesis, atherosclerotic, cardiovascular, cerebrovascular, or

CC	peripheral vascular disease, haemophilia, inflammation and side-effects
CC	from anti-cancer and anti-viral drugs. The vectors can also be used to
CC	create transgenic animals for research or livestock improvement
XX	
SQ	Sequence 3600 BP; 733 A; 1099 C; 1042 G; 726 T; 0 U; 0 Other;
	Query Match 40.9%; Score 2215.8; DB 2; Length 3600;
	Best Local Similarity 99.9%; Pred. No. 7e-276;
	Matches 2217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	3205 CTCAGCTTTTGTTCCTCTTAGTAGGAGGGTAAATTTTCGAGCTTGGCGTAAATCATGTGTCATAG 3264
Db	19 CCCAGCTTTTGTTCCTCTTAGTAGGAGGGTAAATTTTCGAGCTTGGCGTAAATCATGTGTCATAG 78
Qy	3265 CTGTTTCTGTGTGAAATTTGTTATCCCGTCACAATTCACACAATACAGAGCCGGAAGC 3324
Db	79 CTGTTTCTGTGTGAAATTTGTTATCCCGTCACAATTCACACAATACAGAGCCGGAAGC 138
Qy	3325 ATAAAGTGTAAAGCCTGGGTGCTTAATGAGTGAAGCTAACTCAATTAATTGGTTGGCTCGC 3384
Db	139 ATAAAGTGTAAAGCCTGGGTGCTTAATGAGTGAAGCTAACTCAATTAATTGGTTGGCTCGC 198
Qy	3385 TCAGTCGCCGCTTTCAGTTCGGGAAACCTGTCGTCGCCAGCTGCAATTAATGAATCGGCCAA 3444
Db	199 TCAGTCGCCGCTTTCAGTTCGGGAAACCTGTCGTCGCCAGCTGCAATTAATGAATCGGCCAA 258
Qy	3445 CGCGCGGGAGAGCGGTTTTCGCTAATTTGGGCGCTCTTCCGCTTCTCCGCTCACTGACTCG 3504
Db	259 CGCGCGGGAGAGCGGTTTTCGCTAATTTGGGCGCTCTTCCGCTTCTCCGCTCACTGACTCG 318
Qy	3505 CTGGCTCGGTCGTTTCGGCTGCGCGAGCGGTATCAGCTCACTCAAAAGGCGGTAAATACGG 3564
Db	319 CTGGCTCGGTCGTTTCGGCTGCGCGAGCGGTATCAGCTCACTCAAAAGGCGGTAAATACGG 378
Qy	3565 TTATCCACAGATCAGGGGTAAACGACAGGAAGAACATGTGACAAAGGCCGCAAAAG 3624
Db	379 TTATCCACAGATCAGGGGTAAACGACAGGAAGAACATGTGACAAAGGCCGCAAAAG 438
Qy	3625 GCCAGGAACCGTAAAGAGGCGCGTGTCTGGCGTTTTTTCATAGGCTCCGCGCCCTCGTAC 3684
Db	439 GCCAGGAACCGTAAAGAGGCGCGTGTCTGGCGTTTTTTCATAGGCTCCGCGCCCTCGTAC 498
Qy	3685 GAGCATCAAAAAATCGACGCTCAAGTCAGAGTGGGCGAAACCCGACAGGACTATAAAGA 3744
Db	499 GAGCATCAAAAAATCGACGCTCAAGTCAGAGTGGGCGAAACCCGACAGGACTATAAAGA 558
Qy	3745 TACAGAGGTTTCCCGCTGGAGCTCCCTCGTGGCGCTCTCCTGTTCCGACCCCTGCCGCTT 3804
Db	559 TACAGAGGTTTCCCGCTGGAGCTCCCTCGTGGCGCTCTCCTGTTCCGACCCCTGCCGCTT 618
Qy	3805 ACCGGATACCTGTCCGCGTTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGC 3864
Db	619 ACCGGATACCTGTCCGCGTTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGC 678
Qy	3865 TGTTAGGTATCTCAGTTCCGTTAGGTGCTTTCGCTCCAGCTTGGGCTGTGTGACGAACCC 3924
Db	679 TGTTAGGTATCTCAGTTCCGTTAGGTGCTTTCGCTCCAGCTTGGGCTGTGTGACGAACCC 738
Qy	3925 CCGGTTACGCCCGACCGCTGGCCCTTATCCGTTAACTATATGCTTTGAGTCCAAACCCCGGTA 3984
Db	739 CCGGTTACGCCCGACCGCTGGCCCTTATCCGTTAACTATATGCTTTGAGTCCAAACCCCGGTA 798
Qy	3985 AGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTACGACGCGAGCTAT 4044
Db	799 AGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTACGACGCGAGCTAT 858
Qy	4045 GTAGCGGTCGTCACAGAGTTCTTCAAGTGTGGCTTAACCTACGGCTACACTAGAGAACA 4104
Db	859 GTAGCGGTCGTCACAGAGTTCTTCAAGTGTGGCTTAACCTACGGCTACACTAGAGAACA 918
Qy	4105 GTATTTGGTATCTCGGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGTTGGTAGTCTCT 4164
Db	919 GTATTTGGTATCTCGGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGTTGGTAGTCTCT 978

QY 3430 TAATGAATCGGCCAACCGCGGGGAGAGCGGTTTCGGTATTTGGGCGCTCTTCCGCTTCC 3489
DB |||||||
QY 1440 TAATGAATCGGCCAACCGCGGGGAGAGCGGTTTCGGTATTTGGGCGCTCTTCCGCTTCC 1499
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QY 3490 TCGCTCACTGACTCGCTGCGCTCGGTTCGGCTCGCGCGAGCGGTATCAGCTCACTCA 3549
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QY 1680 CTCGCGCCCTCGACGNGCATCAAAAAATCGACGCTCAAGTCAAGAGGTGGCGAAACCCG 1739
DB |||||||
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DB |||||||
QY 1800 CCGACCTGCGCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAGCGTGCGCTT 1859
DB |||||||
QY 3850 TCTCATAGCTCAGCGTGTAGGTATCTCAGTTCGGTGTAGTCCGTCCGCTCCAGCTGGGC 3909
DB |||||||
QY 1860 TCTCATAGCTCAGCGTGTAGGTATCTCAGTTCGGTGTAGTCCGTCCGCTCCAGCTGGGC 1919
DB |||||||
QY 3910 TGTGTGACGAAACCCCGCTTACGCGCGACCGCTGCGCTTATTCGGTAACTATCGTCTT 3969
DB |||||||
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QY 4030 AGCAGAGCAGGTATGTAGCGGTGTCTACAGAGTTCCTGAAGTGGTGGCCCTAACTACGGC 4089
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DB |||||||
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QY 2580 AGTTGCGTGGCGCGAGCCCTTGATGCTCTTGTTCAGATCATCTGTGATCGAACAAGCCG 2639
DB |||||||
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DB |||||||
QY 2640 GCTTCATCCGAGTAGTGTCTCGTCGATCGCATGTTTCGTTGGTGGTTCGATGGGCGAG 2699
DB |||||||
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DB |||||||
QY 2700 GTAGCCGATCAAGCGTATGTCAGCCCGCATTCGATTCAGCCATGATGATATTTCTCG 2759
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QY 2820 TCCCTTCCCGCTTCAGTGAACAAGTTCGACACAGCTGCGCAAGGAAACGCCCGTGTGGCC 2879
DB |||||||
QY 4870 AGCCACGATAGCGCGCTGCTCTCGTCAGTTCATTCAGGGCACCGGACAGGTCCGTC 4929
DB |||||||
QY 2880 AGCCACGATAGCGCGCTGCTCTCGTCAGTTCATTCAGGGCACCGGACAGGTCCGTC 2939
DB |||||||
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DB |||||||
QY 2940 TTGACAAAAAGAAACCGGGCGCCCTCGCTGACAGCGGAAACACGGCGGCGATCAGAGCAG 2999
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QY 4990 CCGATGTTCTGTTGTGCGCCAGTCATAGCCGATAGCTCTCCACCCCAAGCGCGCGAGAA 5049
DB |||||||
QY 3000 CCGATGTTCTGTTGTGCGCCAGTCATAGCCGATAGCTCTCTCCACCCCAAGCGCGCGAGAA 3059
DB |||||||
QY 5050 CTTGCGTGAATCCATCTTTGTTCAATCATGCGAAACGATCCTCATCTGTCTCTTGATCA 5109
DB |||||||
QY 3060 CTTGCGTGAATCCATCTTTGTTCAATCATGCGAAACGATCCTCATCTGTCTCTTGATCA 3119
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QY 5170 CAGGGCTTCCCAACCTTACAGAGGCGCCCGAGCTGGCAATTCGCTTCGCTTGTGCTGTC 5229
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QY 5350 TTTTCCAGTCAAGCTTGTAAAAACGACGCGCCAGTGAATTTGTAATACGACTCACTATAG 5409
DB |||||||
QY 3360 TTTTCCAGTCAAGCTTGTAAAAACGACGCGCCAGTGAATTTGTAATACGACTCACTATAG 3419
DB |||||||
QY 5410 GCGCAATT 5417
DB |||||||
QY 3420 GCGCAATT 3427
DB |||||||

RESULT 12

ABQ78294

ID ABQ78294 standard; DNA; 2192 BP.

XX

AC ABQ78294;

XX

DT 05-NOV-2002 (first entry)

XX

XX 19-JUN-2003.
XX 10-DEC-2002; 2002WO-US039509.
XX 11-DEC-2001; 2001US-0339610P.
XX (ADVI-) ADVISYS INC.
XX (BAYU) BAYLOR COLLEGE MEDICINE.
XX Draghia-Akli R, Carpenter RH, Kern DR, Schwartz RJ, King G;
XX Hahn K, Brenner MK;
XX WPI; 2003-558968/52.
XX Treating anemia, immune dysfunction, tumor, increasing total red blood
XX cell mass, reversing wasting or abnormal weight loss in subject, by
XX administering nucleic acid construct encoding growth-hormone-releasing-
XX hormone.
XX Claim 4; Page 193-195; 212pp; English.
XX The invention relates to compositions and methods for plasmid-mediated
XX supplementation. The method is useful for treating anaemia, tumour (such
XX as adenoma, mast cell tumour, melanoma, sarcoma or solid tumour), immune
XX dysfunction, carcinoma (benign or malignant), leukaemia, lymphoma or
XX kidney failure, for preventing the development of metastatic tumour, for
XX increasing total red blood cell mass, for reversing wasting, abnormal
XX weight loss or suppression of lymphopoesis, in a subject, or for
XX increasing weight gain in a chronically ill subject or, or for extending
XX life expectancy for a chronically ill subject. The present sequence is TV
XX -growth hormone releasing hormone (GHRH) plasmid DNA. This sequence is
XX used to illustrate the method of the invention
XX SQ Sequence 3534 BP; 764 A; 1016 C; 979 G; 775 T; 0 U; 0 Other;
Query Match 39.8%; Score 2160; DB 9; Length 3534;
Best Local Similarity 99.5%; Pred. No. 1e-268;
Matches 2166; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 3190 GAGCCAGGGAACAAGCTCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCG 3249
DB 1359 GAGGGGGGGCCGGTACCAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCG 1418
QY 3250 TAATCATGGTCATAGCTGTTCCCTGTGTGAATTTGTTATCGGCTCACAATTCACACAAC 3309
DB 1419 TAATCATGGTCATAGCTGTTTCTGTGTGAATTTGTTATCGGCTCACAATTTCCACAAC 1478
QY 3310 ATACGAGCCGGAAGCATAAGTGTAAGCCTGGGGTGCCTAATCAGTGAGCTAACTCACA 3369
DB 1479 ATACGAGCCGGAAGCATAAGTGTAAGCCTGGGGTGCCTAATCAGTGAGCTAACTCACA 1538
QY 3370 TTAATTGGTTGCGCTCAGCTCCCGCTTTCCAGTTCGGGAACCTGTGTCGTCAGCTGCAT 3429
DB 1539 TTAATTGGTTGCGCTCAGCTCCCGCTTTCCAGTTCGGGAACCTGTGTCGTCAGCTGCAT 1598
QY 3430 TAATGAATTCGGCCAAACGGCGGGGAGAGCGGGTTGGTATTTGGGGCGCTTTCGCTTCC 3489
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DB 1719 AAGCGGGTAATACGGTTATTCACAGAATCAGGGGATAACCGAGGAAGAAACATGTGAGCA 1778
QY 3610 AAAGCCGAGAAAAGGCCAGGAAACGGTAAAGGCCGGTTCGTGGCGTTTTCATAGG 3669
DB 1779 AAAGCCGAGAAAAGGCCAGGAAACGGTAAAGGCCGGTTCGTGGCGTTTTCATAGG 1838
QY 3670 CTCCGCCCCCTGAGGAGCATCACAAAATTCAGCGCTCAAGCTCAGAGGTGGGAAACCCG 3729

DB 1839 CTCCGCCCCCTGAGGAGCATCACAAAATTCAGCGCTCAAGTCAGAGGTGGGAAACCCG 1898
QY 3730 ACAGGACTATTAAGATACAGGCGTTTCCCTCGGAAGCTCCCTCGTGGCTCTCCTGTT 3789
DB 1899 ACAGGACTATTAAGATACAGGCGTTTCCCTCGGAAGCTCCCTCGTGGCTCTCCTGTT 1958
QY 3790 CCGACCTGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTT 3849
DB 1959 CCGACCTGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTT 2018
QY 3850 TCTCATAGCTCAGCTGTAGGTATCTCAGTTTCGGTGTAGTGTCTCAAGCTCGGC 3909
DB 2019 TCTCATAGCTCAGCTGTAGGTATCTCAGTTTCGGTGTAGTGTCTCAAGCTCGGC 2078
QY 3910 TGTGTGACGAAACCCCGTTTACGCGGACCGCTGGCCCTTATCCCGTAACTACTCGTCT 3969
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QY 3970 GAGTCCAAACCCGGTAAAGACACGACTTATCGCCACTGGCAGCAGCACTGGTAAACAGATT 4029
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QY 4030 AGCAGAGCGAGGTATGTAGCGGTGTCTACAGAGTTCTTGAAGTGGTGGCTTAACACTAGGC 4089
DB 2199 AGCAGAGCGAGGTATGTAGCGGTGTCTACAGAGTTCTTGAAGTGGTGGCTTAACACTAGGC 2258
QY 4090 TACACTAGAAGAACAGTATTTGGTATCTGGCTCTGCTGAAGCCAGTTACTCTTCGAAAA 4149
DB 2259 TACACTAGAAGAACAGTATTTGGTATCTGGCTCTGCTGAAGCCAGTTACTCTTCGAAAA 2318
QY 4150 AGAGTTGGTAGCTCTTGATCCGCAACAAACACACCGCTGCTAGCGGTGGTTTTTTGTT 4209
DB 2319 AGAGTTGGTAGCTCTTGATCCGCAACAAACACACCGCTGCTAGCGGTGGTTTTTTGTT 2378
QY 4210 TGCAAGCAGCAGATTACGCGCAGAAAAAGGATCTCAAGAGATCTTTGATCTTTTCT 4269
DB 2379 TGCAAGCAGCAGATTACGCGCAGAAAAAGGATCTCAAGAGATCTTTGATCTTTTCT 2438
QY 4270 ACGGGTCTGACGCTCAGAGAACTCGTCAAGAGGCGATAGAGCGGATCGGCTCGAA 4329
DB 2439 ACGGGTCTGACGCTCAGAGAACTCGTCAAGAGGCGATAGAGCGGATCGGCTCGAA 2498
QY 4330 TCGGAGCGCGATACCGTAAAGCAGAGGAGCGGTGAGCCATTCGCGCCCAAGCTCT 4389
DB 2499 TCGGAGCGCGATACCGTAAAGCAGAGGAGCGGTGAGCCATTCGCGCCCAAGCTCT 2558
QY 4390 TCAGCAATATCAGGGTAGCCAAACGCTATGTCTGTAGTGGTCCGCCACACCCAGCGG 4449
DB 2559 TCAGCAATATCAGGGTAGCCAAACGCTATGTCTGTAGTGGTCCGCCACACCCAGCGG 2618
QY 4450 CCACAGTCGATGAATCCAGAAAAAGCGCCATTTTCCACCATGATATTTCCGCAAGCAGCA 4509
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DB 2859 GTAGCCGGATCAAGCGTATGAGCGCGCGCATTCGATCAGCCATGATGATCTTTCTCG 2918
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[illegible]

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Db	3339	CAGGGCTTCCCAACCTTTACAGAGGGCGCCCCAGCTGGCAATTCGGTTCGCTGTGCTGTC	3398
Qy	5230	CATAAAACCGGCCAGTCTAGCAACTGTTGGGAAGGGCGATCGGTGCGGGGCTCTTCGCTA	5289
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Qy	5290	TTACGCAGCTGGCGAAAGGGGGATGTCTGCAAGGCGATTAAAGTTGGGTAAACGCCAGGG	5349
Db	3459	TTACGCAGCTGGCGAAAGGGGGATGTCTGCAAGGCGATTAAAGTTGGGTAAACGCCAGGG	3518
Qy	5350	TTTTTCCAGTCACGAC	5365
Db	3519	TTTTTCCAGTCACGAC	3534

Search completed: February 20, 2006, 19:34:42
Job time : 2802 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 18:57:52 ; Search time 19467 Seconds
(without alignments)
13033.665 Million cell updates/sec

Title: US-10-798-896-1

Perfect score: 5423

Sequence: 1 ccaccgcgtgcccgcgc.....ctataggcgcaattggagct 5423

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hic:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gss1:*

10: gb_gss2:*

11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1006.8	18.6	1186	DR045845	FP-10_F08
2	992.4	18.3	1176	CK943193	LamjGestG
3	987.2	18.2	1067	AU081137	AU081137
4	959	17.7	1089	AU081124	AU081124
5	903.2	16.7	1049	CL021189	CH216-8A1
6	901	16.6	925	CB686151	Bn01b_020
7	893.2	16.5	1191	DR045882	FP-11_A09
8	859.2	15.8	885	CL076016	CH216-138
9	853	15.7	1195	DR046031	FP-8_F02
10	852.8	15.7	951	CV983341	UMC-bof_0
11	852.6	15.7	875	CK012952	io62d12_b
12	835.6	15.4	1073	CF269652	Fyqlcd8
13	824.4	15.2	1169	AG332951	Mus muscu
14	823.2	15.2	1025	CL021193	CH216-8A1
15	820.4	15.1	1163	AU081044	AU081044
16	818.8	15.1	868	CV984340	UMC-bov_0
17	812.6	15.0	935	CK284786	EST747508
18	804.8	14.8	833	CB686421	Bn01b_04j
19	803.6	14.8	966	BZ570738	msH2_1513
20	800.4	14.8	804	CV979032	UMC-Bemiv
21	798.6	14.7	813	CK006605	io23f10_b
22	796	14.7	804	CK291519	EST754233

c	23	796	14.7	856	7	CK287297	CK287297	EST750019
c	24	796	14.7	910	7	CK287930	CK287930	EST750652
c	25	796	14.7	933	7	CK291799	CK291799	EST754513
c	26	796	14.7	936	7	CK256977	CK256977	EST740614
c	27	796	14.7	947	7	CK298208	CK298208	EST760922
c	28	796	14.7	954	7	CK283361	CK283361	EST746083
c	29	794	14.6	811	7	CK288185	CK288185	EST750907
c	30	788.4	14.5	886	8	DN818689	DN818689	UMC-bconb
c	31	786.2	14.5	865	7	CK125894	CK125894	BES182411
c	32	783.4	14.4	833	8	CK013029	CK013029	io62h07_b
c	33	779.4	14.4	846	7	CV468077	CV468077	est_l_van
c	34	777.9	14.4	841	8	CK011012	CK011012	io49h10_b
c	35	778.8	14.4	894	8	DN641029	DN641029	UMC-bend
c	36	777.6	14.3	1164	8	DR045996	DR045996	FP-8_C03
c	37	775.8	14.3	1194	9	BZ578985	BZ578985	msH2_6095
c	38	774	14.3	954	1	AL044364	AL044364	DKF2P434C
c	39	773.4	14.3	776	8	CK006479	CK006479	io23a02_b
c	40	772.2	14.2	808	8	CK006965	CK006965	io25f10_b
c	41	769.2	14.2	863	6	CF752100	CF752100	TGDR9_Hum
c	42	762.2	14.1	814	8	CK008423	CK008423	io34d12_b
c	43	762	14.1	1249	9	BZ572284	BZ572284	msH2_2572
c	44	761.4	14.0	959	9	BZ557985	BZ557985	pacs1-60
c	45	761	14.0	761	8	CK008002	CK008002	io31f11.5

ALIGNMENTS

RESULT 1	DR045845	1186 bp	linear	EST 02-JUN-2005
LOCUS	FP-10_F08	SEQ cDNA library of Phaeosphaeria nodorum grown on wheat cell walls	Phaeosphaeria nodorum cDNA, mRNA sequence.	
DEFINITION	DR045845	1 GI:66909681		
ACCESSION	DR045845			
VERSION	EST.			
KEYWORDS	Phaeosphaeria nodorum			
SOURCE	Phaeosphaeria nodorum			
ORGANISM	Phaeosphaeria nodorum			
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes; Pleosporales; Phaeosphaeriaceae; Phaeosphaeria.			
AUTHORS	1 (bases 1 to 1186)			
TITLE	Bindschedler, L.V., Cooper, R.M., Thomas, S.W., Madrid, M.P. and Oliver, R.P.			
JOURNAL	cDNA library of Phaeosphaeria nodorum grown on Wheat cell walls			
COMMENT	Unpublished (2005)			
	Contact: Richard Oliver			
	Australian Centre for Necrotrophic Fungal Pathogens (ACNFP)			
	Murdoch University			
	South Street, Murdoch, W.A 6150, Australia			
	Tel: +0893607404			
	Email: roliver@murdoch.edu.au.			

FEATURES	Location/Qualifiers
source	1..1186
	/organism="Phaeosphaeria nodorum"
	/mol_type="mRNA"
	/db_xref="taxon:13684"
	/clone_lib="cDNA library of Phaeosphaeria nodorum grown on wheat cell walls"

ORIGIN

Query Match	18.6%;	Score	1006.8;	DB	8;	Length	1186;
Best Local Similarity	98.2%;	Pred. No.	1.6e-276;				
Matches	1039;	Conservative	0;	Mismatches	17;	Indels	2;
Gaps	2;						
QY	3248	CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTTATCCGCTCACAAATTCACACA	3307				
Db	23	CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTTATCCGCTCACAAATTCACACA	82				
QY	3308	ACATAGACCCGGAACATAGTGTAAAGCCCTGGGCTTAATGAGTGAGCTAACTCA	3367				
Db	83	ACATAGACCCGGAACATAGTGTAAAGCCCTGGGCTTAATGAGTGAGCTAACTCA	142				
QY	3368	CATTAATTGGTTGCGCTCACTCCCGCTTTCAGTCGGGAAACCTGTCTGTCAGCTGC	3427				

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Db 143 CATTAAATGCGTGTGCGCTCACTGCGCGCTTTCCAGTCGGGAACCTGTCGTGCGAGCTGC 202
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Qy 3488 CCTCGCTCACTGACTGCTGCGCTCGGTCGCTTGGCTTGGCGGCGAGCGGTATCAGCTCACT 3547
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Qy 3608 CAAAGGCGCAAAAGGCGCAGGAACCGTAAAGGCGGTTGCTGGCGCTTTTCCATA 3667
Db 383 CAAAGGCGCAAAAGGCGCAGGAACCGTAAAGGCGGTTGCTGGCGCTTTTCCATA 442
Qy 3668 GGCTCCGCCCCCTGACGAGCATCACAAAATCGAGCTCAAGTTCAGAGTGGCGAAACC 3727
Db 443 GGCTCCGCCCCCTGACGAGCATCACAAAATCGAGCTCAAGTTCAGAGTGGCGAAACC 502
Qy 3728 CGACGAGCTATAAGATACACGCGGTTTCCCGCTGGAAGCTCCCTCGTGGCTCTCCTG 3787
Db 503 CGACGAGCTATAAGATACACGCGGTTTCCCGCTGGAAGCTCCCTCGTGGCTCTCCTG 562
Qy 3788 TTCCGACCTGCGCGCTTACCGGATACCTGTGCGGCTTTCCTTCCCTTCGGGAAGCGTGGCGC 3847
Db 563 TTCCGACCTGCGCGCTTACCGGATACCTGTGCGGCTTTCCTTCCCTTCGGGAAGCGTGGCGC 622
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Qy 3908 GCTGTGTGCAAGAACCCCGGTTTCAGCCGACCGCTGCGGCTTATCCGGTAACTATCGTC 3967
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Qy 4088 GCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAAGCCAGTTACCTTCGGAA 4147
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Qy 4148 AAGAGTTGGTAGCTCTTGTATCCGGCAACAAACACCGCTGTTAGCGGTGGTTTTTTTG 4207
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Qy 4208 TTTTCAGAGCGAGTATTAACGGCGAGAAAGAGATCTCAAGAGATCTTTCATCTTTT 4267
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Qy 4268 CTACGGGCTGACGCTTCAGAAGAACTCTGTCAGAAAGG 4305
Db 1041 TCTACGGGCTGACGCTTCAGTGACAAACTCACGTAGG 1078
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RESULT 2
CX943193
LOCUS CX943193 1176 bp mRNA linear EST 09-FEB-2005
DEFINITION LamJestGS8 Laminaria japonica Lambda Zap Express Library Laminaria
japonica cDNA 5', mRNA sequence.
ACCESSION CX943193
VERSION CX943193.1 GI:58802440
KEYWORDS EST.
SOURCE Laminaria japonica
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ORGANISM Laminaria japonica
Bukaryota; Stramenopiles; Phaeophyceae; Laminariales;
Laminariaceae; Laminaria.
REFERENCE 1 (bases 1 to 1176)
AUTHORS Xuan,J., Zhao,G., Wang,W., Duan,D., Weng,M. and Wang,B.
TITLE Expressed sequence tag analysis of the brown alga Laminaria
japonica (Phaeophyceae)
JOURNAL Unpublished (2005)
COMMENT Contact: Xuan JS
The State Key Laboratory of Plant Genome Research
Institute of Genetics and Developmental Biology, Chinese Academy of
Science
Datun Road, Chaoyang District, Beijing, China, 100101
Tel: 086 010 64889353
Fax: 086 010 64873428
Email: bnxuan@hotmail.com
Seq primer: T3 Forward
High quality sequence stop: 1176.
FEATURES
Location/Qualifiers
source 1..1176
/organism="Laminaria japonica"
/mol_type="mRNA"
/db_xref="taxon:88149"
/sex="female"
/dev_stage="gametophyte"
/clone_lib="Laminaria japonica Lambda Zap Express Library"
/note="Vector: Uni-ZAP@ XR vector; Site_1: EcoRI; Site_2:
XhoI"
ORIGIN
Query Match 18.3%; Score 992.4; DB 8; Length 1176;
Best Local Similarity 99.0%; Pred. No. 2.2e-272;
Matches 1030; Conservative 0; Mismatches 6; Indels 4; Gaps 3;
Qy 3248 CGTAATCATGTCATAGCTGTTTCCCTGTGTGAAATTTTATCCGCTCACAATTCACACA 3307
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Db 157 CATTAAATGCTGTCGCTCACTGCCGCTTTTCCAGTCGGGAAACCTGTCTGTCAGCTGC 216
Qy 3428 ATTAATGAATCGGCCAAACGCGCGGAGAGCGGTTTGGTATTTGGCGCTCTTCCGCTT 3487
Db 217 ATTAATGAATCGGCCAAACGCGCGGAGAGCGGTTTGGTATTTGGCGCTCTTCCGCTT 276
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Qy 3668 GGCTCCGCCCCCTGACGAGCATCACAAAATCGAGCTCAAGTTCAGAGTGGCGAAACC 3727
Db 457 GGCTCCGCCCCCTGACGAGCATCACAAAATCGAGCTCAAGTTCAGAGTGGCGAAACC 516
Qy 3728 CGACGAGCTATAAGATACACGCGGTTTCCCGCTGGAAGCTCCCTCGTGGCTCTCCTG 3787
Db 517 CGACGAGCTATAAGATACACGCGGTTTCCCGCTGGAAGCTCCCTCGTGGCTCTCCTG 576
Qy 3788 TTCCGACCTGCGCTTACCGGATACCTGTGCGGCTTTTCCCTTCGGGAAGCGTGGCGC 3847
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QY 3908 GCTGTGTGACGAACCCCGTTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTC 3967
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QY 3968 TTGAGTCCAAACCGGTGAAGACAGACTTATCGCACCTGGCAGCAGCCACTGGTAAACAGGA 4027
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QY 4028 TTAGCAGAGCGAGTATGTAGGCGGTGCTACAGAGTTCTTTGAAGTGTGTGCGCTTAACCTACG 4087
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QY 4088 GCTACACTAGAAGAACAGTATTTGGTATCTGCGCTGCTGTAAGCCAGTTACCTTGGAA 4147
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QY 4148 AAAGAGTTGTAGTCTTTGATCGGCAAAACAAACCCGCTGCTGAGCGGTGTTTTTTTG 4207
DB 937 AAAGAGTTGTAGTCTTTGATCGGCAAAACAAACCCGCTGCTGAGCGGTGTTTTTTTG 995
QY 4208 TTTGCAAGCAGCAGATTACGCGCAGAAAAAAGAGATCTCAAGAGATCTTTTATCTTTT 4267
DB 996 TTTGCAAGCAGCAGATTACGCGCAGAAAAA--GGATCTCAGAAGATCTTTGATCTTTT 1053
QY 4268 CTAGCGGTCTGAGCTCAG 4287
DB 1054 CTAC-GGGTCTGAGCTCAG 1072

RESULT 3
AU081137
LOCUS
DEFINITION
hematopoietic necrosis virus Oncorhynchus mykiss kidney infected by infectious
mRNA sequence.
ACCESSION
AU081137.1 GI:6431485
VERSION
EST.
KEYWORDS
Oncorhynchus mykiss (rainbow trout)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE
1 (bases 1 to 1067)
Kono,T., Sakai,M. and LaPatra,S.E.
Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
Hematopoietic Necrosis Virus
Mar. Biotechnol. 2 (5), 493-498 (2001)
CONTACT: Masahiro Sakai
Faculty of Agriculture
Miyazaki University
1-1 nishi gakukenibandai, Miyazaki, Miyazaki 889-2192, Japan
Email: m.sakai@cc.miyazaki-u.ac.jp.
FEATURES
Source
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/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="KI2"
/tissue_type="kidney"
/clone_lib="Oncorhynchus mykiss Kidney infected by
infectious hematopoietic necrosis virus"
/note="common name:rainbow trout ; infected by infectious
hematopoietic necrosis virus"

Query Match 18.2%; Score 987.2; DB 1; Length 1067;
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Best Local Similarity 99.0%; Pred. No. 6.6e-271;
Matches 1014; Conservative 0; Mismatches 8; Indels 2; Gaps 2;
QY 3207 CAGCTTTTGTTCCTTTTAGTGAGGGTTAAATTCGAGCTTGGCGCTTAATCATGGTCATAGCT 3266
DB 46 CAGCTTTTGTTCCTTTTAGTGAGGGTTAAATTCGAGCTTGGCGCTTAATCATGGTCATAGCT 105
QY 3267 GTTTCCTGTGTGAAATTTGTATCCGCTCAAAATTCACAAATACGAGCCGGAAGCAT 3326
DB 106 GTTTCCTGTGTGAAATTTGTATCCGCTCAAAATTCACAAATACGAGCCGGAAGCAT 165
QY 3327 AAAGTGAAGCCCTGGGGTCCCTAATGAGTGAGCTAACTCACATTAAATTCGGTTGCCCTC 3386
DB 166 AAAGTGAAGCCCTGGGGTCCCTAATGAGTGAGCTAACTCACATTAAATTCGGTTGCCCTC 225
QY 3387 ACTGCCCGCTTTCAGTTCGGGAAACCTGTCGTCAGCTGCATTAATGAATCGGCCAAGC 3446
DB 226 ACTGCCCGCTTTCAGTTCGGGAAACCTGTCGTCAGCTGCATTAATGAATCGGCCAAGC 285
QY 3447 CGCGGGGAGAGCGGTTTTCGTTATTTGGCGCTCTTCGCTTTCCTCGCTCACTGACTCGCT 3506
DB 286 CGCGGGGAGAGCGGTTTTCGTTATTTGGCGCTCTTCGCTTTCCTCGCTCACTGACTCGCT 345
QY 3507 GCGCTCGGTCTGCGGTGCGGCGAGCGGTATCAGCTCACTCAAGCGGCTAATACGGTT 3566
DB 346 GCGCTCGGTCTGCGGTGCGGCGAGCGGTATCAGCTCACTCAAGCGGCTAATACGGTT 405
QY 3567 ATCCACAGAAATCAGGGGATAACCGCAGGAAAGAAATGTGAGCAAAAGGCCAGCAAAAGGC 3626
DB 406 ATCCACAGAAATCAGGGGATAACCGCAGGAAAGAAATGTGAGCAAAAGGCCAGCAAAAGGC 465
QY 3627 CAGGAAACCGTAAAGAGCGCGGTTGCTGGCGTTTTCATAGGCTCCGCCCTCCCTGACGA 3686
DB 466 CAGGAAACCGTAAAGAGCGCGGTTGCTGGCGTTTTCATAGGCTCCGCCCTCCCTGACGA 525
QY 3687 GCATCAAAAATTCGAGCTCAAGTCAGAGGTGGGAAACCCGACAGGACTATAAGATA 3746
DB 526 GCATCAAAAATTCGAGCTCAAGTCAGAGGTGGGAAACCCGACAGGACTATAAGATA 585
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DB 586 CAGGCGGTTTCCCGCTGGAAGCTCCCTCGTGGCGCTCTCCTGTTCCGACCTGCCGCTTAC 645
QY 3807 CGGATACCTGTCCGCCCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTG 3866
DB 646 CGGATACCTGTCCGCCCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTG 705
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DB 706 TAGGTATCTCAGTTCCGGTGTAGTGTGCTCCAGCTGGGCTGTGTGACGAAACCCCTC 765
QY 3927 CGTTAGCCCGACCGCTGCGCTTATCCGCTAACTATCGTCTTGAGTCCAAACCCGGTAAG 3986
DB 766 CGTTAGCCCGACCGCTGCGCTTATCCGCTAACTATCGTCTTGAGTCCAAACCCGGTAAG 825
QY 3987 ACAGGACTTATCCGCCACTGGCAGCAGCACTGGTAAACAGGATTAGCAGAGCGAGTATGT 4046
DB 826 ACAGGACTTATCCGCCACTGGCAGCAGCACTGGTAAACAGGATTAGCAGAGCGAGTATGT 885
QY 4047 AGCGGTGTACAGAGTTCTTGAAGTGTGGTCCCTTAACCTAGGCTACACTAGAGAAACAGT 4106
DB 886 AGCGGTGTGTACAGAGTTCTTGAAGTGTGGTCCCTTAACCTAGGCTACACTAGAGAAACAGT 945
QY 4107 ATTGTGTATCTCGCTCTGCTGTAAGCCAGTTACCTTCGGAAAAAGAGTTCGTAGCTCTTG 4166
DB 946 ATTGTGTATCTCGCTCTGCTGTAAGCCAGTTTACCTTCGGAAAAAGAGTTCGTAGCTCTTG 1005
QY 4167 ATCCGCAAAACAAACCCAGCTGTAGCGGTGTTTTTTTTTTGTTGCAAGCAGCAGATTAC 4226
DB 1006 ATCCGCAAAACAAAC--CAACGCTGTAGCGGTGTTTTTTTTTTGTTGTC--AGCAGCAGATTAC 1063
QY 4227 GCGC 4230
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Db      1064 GC GC 1067

RESULT 4
AU081124
LOCUS   AU081124
DEFINITION AU081124 Oncorhynchus mykiss 1089 bp mRNA linear EST 30-JUL-2002
hematopoietic necrosis virus Oncorhynchus mykiss cDNA clone KG/12,
mRNA sequence.
ACCESSION AU081124
VERSION   AU081124.1 GI:6431472
SOURCE   EST.
ORGANISM Oncorhynchus mykiss (rainbow trout)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1 (bases 1 to 1089)
AUTHORS   Kono,T., Sakai,M. and LaPatra,S.E.
TITLE     Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
Hematopoietic Necrosis Virus
JOURNAL   Mar. Biotechnol. 2 (5), 493-498 (2001)
COMMENT   Contact: Masahiro Sakai
Miyazaki University
1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan
Email: m.sakai@cc.miyazaki-u.ac.jp.
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infectious hematopoietic necrosis virus"
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hematopoietic necrosis virus"

ORIGIN
Query Match      17.7%; Score 959; DB 1; Length 1089;
Best Local Similarity 97.5%; Pred. No. 8.2e-263;
Matches 1017; Conservative 0; Mismatches 20; Indels 6; Gaps 4;

QY      3207 CAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCGTAATCATAGCT 3266
Db      |||||||
QY      47 CAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCGTAATCATAGCT 106
Db      |||||||
QY      3267 GTTTCCTGTGTGAATTTGTTATCCGCTCACAATTTCCACACATACGAGCCGGAAGCAT 3326
Db      |||||||
QY      107 GTTTCCTGTGTGAATTTGTTATCCGCTCACAATTTCCACACATACGAGCCGGAAGCAT 166
Db      |||||||
QY      3327 AAAGTGAAGCCCTGGGGTGCTTAATGAGTGAGTAACTCACAATTAATGGTTGCGCTC 3386
Db      |||||||
QY      167 AAAGTGAAGCCCTGGGGTGCTTAATGAGTGAGTAACTCACAATTAATGGTTGCGCTC 226
Db      |||||||
QY      3387 ACTGCCGCTTTTCAGTCGCGGAACCTGTGTCGACGTCGATTAATGAATCGGCCAACG 3446
Db      |||||||
QY      227 ACTGCCGCTTTTCAGTCGCGGAACCTGTGTCGACGTCGATTAATGAATCGGCCAACG 286
Db      |||||||
QY      3447 CGCGGGGAGAGCGGTTTGGTATTTGGCGGCTCTTCGCTTCCTCGCTCACTGACTCGCT 3506
Db      |||||||
QY      287 CGCGGGGAGAGCGGTTTGGTATTTGGCGGCTCTTCGCTTCCTCGCTCACTGACTCGCT 346
Db      |||||||
QY      3507 GCGCTCGCTGCTTCGCGTGGCGGAGGGTATCAGCTCACTCAAGGCGGTAATACGGTT 3566
Db      |||||||
QY      347 GCGCTCGCTGCTTCGCGTGGCGGAGGGTATCAGCTCACTCAAGGCGGTAATACGGTT 406
Db      |||||||
QY      3567 ATCCACAGATCATCGGGGATTAACGAGGAAGAAATGTGAGCAAAAGCCAGCAAAAGGC 3626
Db      |||||||
QY      407 ATCCACAGATCATCGGGGATTAACGAGGAAGAAATGTGAGCAAAAGCCAGCAAAAGGC 466
Db      |||||||

QY      3627 CAGGAACCGTAAAGCGCGGTTGCTGGGTTTTTCCATAGGCTCGGCCCTCGACGA 3686
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QY      467 CAGGAACCGTAAAGCGCGGTTGCTGGGTTTTTCCATAGGCTCGGCCCTCGACGA 526
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QY      3687 GATCACAAAAATCGAGGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATA 3746
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QY      527 GATCACAAAAATCGAGGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATA 586
Db      |||||||
QY      3747 CAGGCGGTTTTCCCTCGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCTGCGGCTTAC 3806
Db      |||||||
QY      587 CAGGCGGTTTTCCCTCGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCTGCGGCTTAC 646
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QY      3807 CGGATACCTGTGCGGCTTTCTCCCTTCGGGAAGCTGGGCGCTTTCTCATAGCTCACGCTG 3866
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QY      647 CGGATACCTGTGCGGCTTTCTCCCTTCGGGAAGCTGGGCGCTTTCTCATAGCTCACGCTG 706
Db      |||||||
QY      3867 TAGGTATCTCAGTTCGGTGTAGTGTGCTCCAGCTGGGCTGTGTGACGAACCCCC 3926
Db      |||||||
QY      707 TAGGTATCTCAGTTCGGTGTAGTGTGCTCCAGCTGGGCTGTGTGACGAACCCCC 766
Db      |||||||
QY      3927 CGTTCAGCCGACCGCTGCGCTTATCCGCTAACTATCGTCTTGAAGTCCAAACCGGTAAG 3986
Db      |||||||
QY      767 CGTTCAGCCGACCGCTGCGCTTATCCGCTAACTATCGTCTTGAAGTCCAAACCGGTAAG 826
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Db      |||||||
QY      887 AGCGGCTGTACAGAGTTCTTGAAGTTTGTGGCTTAACCTACGCGTACACTAGAGAAGCAG 946
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QY      4166 -GATCCGGCAAAACAAACCA---CCGCTGTAGCGGTGGTGTGTGTTTGTTCGAAGCA-GCA 4220
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QY      1007 GGATCCGGCAAAACAAACACACCGCTGGGAAGGGGGTGTCCTTTTGTTCGAAGCAGCA 1066
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QY      4221 GATTACGCGCAGAAACAAAGGAT 4243
Db      |||||||
QY      1067 GATTACGCGCAGAAACAAACCGAT 1089
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RESULT 5
CL021189
LOCUS   CL021189
DEFINITION CL021189 RM1.1 CH216 Xenopus tropicalis genomic clone CH216-8A14,
genomic survey sequence.
ACCESSION CL021189
VERSION   CL021189.1 GI:40463002
KEYWORDS  GSS.
SOURCE    Xenopus tropicalis (western clawed frog)
ORGANISM  Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 1049)
AUTHORS   Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,R.
TITLE     A physical map of the xenopus tropicalis genome
JOURNAL   Unpublished (2003)
COMMENT   Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: RM1 TAGCACTCACTATAGGAGA
Class: BAC ends
High quality sequence start: 43
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Location/Qualifiers

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/sex="male"
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BAC library"

ORIGIN
Query Match 16.7%; Score 903.2; DB 10; Length 1049;
Best Local Similarity 98.4%; Pred. No. 8.5e-247;
Matches 933; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

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DB 101 TGCAGGCTTGGCGTAATCATGTCATAGCTGTTTCTCTGTGTGAATTTATCCGCTCAC 160

QY 3297 AATTCCACACATACGAGCGGAGCATAAAGTGTAAAGCTCGGGTGCCCTAATGAGT 3356
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QY 3357 GAGCTAACTCACATTAATTGCGTTGGCTCAGTCCCGCTTTCCAGTCGGGAAACCTGTG 3416
DB 221 GAGCTAACTCACATTAATTGCGTTGGCTCAGTCCCGCTTTCCAGTCGGGAAACCTGTG 280

QY 3417 GTGCCAGCTGCATTAATGAAATGGCCAAACGCGGGGAGAGCGGTTTGGCTAATGGCG 3476
DB 281 GTGCCAGCTGCATTAATGAAATGGCCAAACGCGGGGAGAGCGGTTTGGCTAATGGCG 340

QY 3477 CTCTTCGCTTCTCGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3536
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QY 3537 ATCAGCTCACTCAAAGCGGTAATACGTTTATCCACAGATCAGGGGATAAACGAGAA 3596
DB 401 ATCAGCTCACTCAAAGCGGTAATACGTTTATCCACAGATCAGGGGATAAACGAGAA 460

QY 3597 GAACATGTGAGCAAAAGCGCAGCAAAAGCGCAGAAACCGTAAAGAGCGCGTTGTGCG 3656
DB 461 GAACATGTGAGCAAAAGCGCAGCAAAAGCGCAGAAACCGTAAAGAGCGCGTTGTGCG 520

QY 3657 GTTTTTCATAGGCTCGCCCTCAGCAGCATCAAAAATCGAGCTCAAGTCAGAG 3716
DB 521 GTTTTTCATAGGCTCGCCCTCAGCAGCATCAAAAATCGAGCTCAAGTCAGAG 580

QY 3717 GTGGCAAAACCCGACAGGACTATAAGATACAGGCGTTTCCCGCTGGAAGCTCCCTCGT 3776
DB 581 GTGGCAAAACCCGACAGGACTATAAGATACAGGCGTTTCCCGCTGGAAGCTCCCTCGT 640

QY 3777 GGGCTCTCGTTTCGACCGCTGCGCTTACCGGATACCTGTGCGCTTTCTCCCTTCGG 3836
DB 641 GGGCTCTCGTTTCGACCGCTGCGCTTACCGGATACCTGTGCGCTTTCTCCCTTCGG 700

QY 3837 AAGCGTGGCGCTTCTCATAGCTCAGCTGTAGTATCTCAGTTCCGTTAGTGTGCTTGC 3896
DB 701 AAGCGTGGCGCTTCTCATAGCTCAGCTGTAGTATCTCAGTTCCGTTAGTGTGCTTGC 760

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QY 3957 TAACTATCGTTTGTAGTCAACCCCGTAAAGACACGACTTATGCCACTGCGCAGCCAC 4016
DB 821 TAACTATCGTTTGTAGTCAACCCCGTAAAGACACGACTTATGCCACTGCGCAGCCAC 880

QY 4017 TGGTAACAGGATTAGCAGAGCGAGGATGTAGGCGGTGTCTACAGATTCTTGAAGTGGTG 4076
DB 881 TGGTAACAGGATTAGCAGAGCGAGGATGTAGGCGGTGTCTACAGATTCTTGAAGTGGTG 940

QY 4077 GCCTAACTACGGCTACACTAGAGAAC-AGTATTTGGTATCTCGCTCTCTGTAAGCCAG 4135
DB 941 GCCTAACTACGGCTACACTAGAGAACAGTATTTGGTATCTCGCTCTCTGTAAGCCAG 1000

QY 4136 TTACC-TTCGGAAGAGTGTGCTCTCTGATCCGGCAACAAACC 4182
DB 1001 TTACC-TTCGGAAGAGTGTGCTCTCTGATCCGGCAACAAAC 1048

RESULT 6
CB686151/c 925 bp mRNA linear EST 09-APR-2003
LOCUS Bn01b_02008 A
DEFINITION Bn01b AAFECORC transgenic Brassica napus overexpressing BNCBF17 c
onstitutively_frost_tolerant Brassica napus cDNA clone Bn01b_02008,
mRNA sequence.
ACCESSION CB686151 GI:29689876
VERSION CB686151.1
SOURCE EST.
ORGANISM Brassica napus (rape)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 925)
AUTHORS Singh, J., Allard, G., Tinker, N., Robert, L., Lacroix, C., De Moors, A.,
Chagnon, J., Farah, S., Couroux, P. and Hattori, J.
TITLE Expressed Sequence Tags from constitutively frost tolerant
transgenic Brassica napus overexpressing BNCBF17
JOURNAL Contact: Singh, J.A.
COMMENT Unpublished (2002)
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-Food Canada
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
0C6, Canada
Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@agr.gc.ca.
FEATURES
Location/Qualifiers
1..925
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Westar"
/db_xref="taxon:3708"
/clone="Bn01b_02008"
/tissue_type="fourth leaf"
/dev_stage="3 weeks seedling grown at room temperature"
/clone_lib="Bn01b AAFECORC transgenic Brassica napus_ove
rexpressing BNCBF17 constitutively frost tolerant"
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI;
Site 2: XhoI; Germinated in soil flats and seedlings grown
for 3 weeks in a Conviron E-15 cabinet set at 20°C/16 hr
light (250 Em-2sec-1) and 16 °C/ 8 hr dark. Fourth leaves
collected at 9 am and immediately frozen."

ORIGIN
Query Match 16.6%; Score 901; DB 6; Length 925;
Best Local Similarity 98.6%; Pred. No. 3.5e-246;
Matches 912; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 3212 TTGTGTCCCTTTAGTGAGGTTAATTTTCGAGCTTGGCGTAATCATGCTCATAGCTGTTTC 3271
DB 924 TTGTGTCCCTTTAGTGAGGTTAATTTTCGCGCTTGGCGTAATCATGCTCATAGCTGTTT - 866

QY 3272 CTGTGTGAATTTGTTATCCGCTCAAAATTCACAAATACAGCGCGGAAGCATAAAGT 3331
DB 865 CTGTGTGAATTTGTTATCCGCTCAAAATTCACAAATACAGCGCGGAAGCATAAAGT 806

QY 3332 GTAAAGCCTGGGTCCTAATGAGTGAGCTACTCATTAATTTGCGTCTCACTGC 3391
DB 805 GTAAAGCCTGGGTCCTAATGAGTGAGCTACTCATTAATTTGCGTCTCACTGC 746

QY 3392 CGGCTTTTCAGTCGGGAAACCTGTGTCGAGCTGATTAATGAATCGGCCAACGGCGG 3451
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Db 745 CCGCTTCAGTCGGGAACCTGTCGTCCAGCTGCTAATTAATGAATCGGCAACGCGCG 686
Qy 3452 GGAGAGCGGTTGGCGTATGGCGCGCTTTCGCGCTTCCTCGCTCACTGACTCGCTCGCT 3511
Db 685 GGAGAGCGGTTGGCGTATGGCGCGCTTTCGCGCTTCCTCGCTCACTGACTCGCTCGCT 626
Qy 3512 CGGTCTCGGTGGCGCGGCGATATGAGTCACTCAAAAGGCGGTAATACGGTTATCCA 3571
Db 625 CGGTCTCGGTGGCGCGGCGATATGAGTCACTCAAAAGGCGGTAATACGGTTATCCA 566
Qy 3572 CAGAATCAGGGGATAACGCGAGGAAGAAACATGTGAGCAAAAGCCAGCAAAAGCCAGGA 3631
Db 565 CAGAATCAGGGGATAACGCGAGGAAGAAACATGTGAGCAAAAGCCAGCAAAAGCCAGGA 506
Qy 3632 ACCGTAAAAGGCGGCTGCTGGCGTTTTCATAGGCTCCGCGCCCTCGAGCAGATC 3691
Db 505 ACCGTAAAAGGCGGCTGCTGGCGTTTTCATAGGCTCCGCGCCCTCGAGCAGATC 446
Qy 3692 ACAAAATCAGCCTCAAGTCAGAGTGGCGAAACCGCAGCAGACTATAAAGATACCAGG 3751
Db 445 ACAAAATCAGCCTCAAGTCAGAGTGGCGAAACCGCAGCAGACTATAAAGATACCAGG 386
Qy 3752 CGTTTCCCTCGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCCTGCGCTTACCGGAT 3811
Db 385 CGTTTCCCTCGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCCTGCGCTTACCGGAT 326
Qy 3812 ACTGTCCGCTTTCCTCCGGAAGCGTGGCGCTTTCATAGCTACGCTGATAGT 3871
Db 325 ACTGTCCGCTTTCCTCCGGAAGCGTGGCGCTTTCATAGCTACGCTGATAGT 266
Qy 3872 ATCTCAGTTCCGTTAGTTCGCTCCAGCTGGCTGTGTCAGCAACCCCGCTTC 3931
Db 265 ATCTCAGTTCCGTTAGTTCGCTCCAGCTGGCTGTGTCAGCAACCCCGCTTC 206
Qy 3932 AGCCGACCGCTGGCTTATCCGTAACCTATCGTCTTGAGTCCAAACCCCGTAAGCACG 3991
Db 205 AGCCGACCGCTGGCTTATCCGTAACCTATCGTCTTGAGTCCAAACCCCGTAAGCACG 146
Qy 3992 ACTTATCGCACTGGCAGCAGCACTGGTAACAGGATTAGCAGCAGGATGTAGGCG 4051
Db 145 ACTTATCGCACTGGCAGCAGCACTGGTAACAGGATTAGCAGCAGGATGTAGGCG 86
Qy 4052 GTGCTACAGATTCCTGAAGTGGCTTAACCTACGCTACACTAGAGACAGATTTTG 4111
Db 85 GTGCTACAGATTCCTGAAGTGGCTTAACCTACGCTACACTAGAGACAGATTTTG 26
Qy 4112 GTATCTCGCTCTGCTGAAGCCAGT 4136
Db 25 GTATCTCGCTCTGCTGAAGCCAGT 1

RESULT 7
DR045882
LOCUS 1191 bp mRNA linear EST 02-JUN-2005
DEFINITION FP-11_A09.SEQ cDNA library of Phaeosphaeria nodorum grown on wheat
cell walls Phaeosphaeria nodorum cDNA, mRNA sequence.
ACCESSION DR045882
VERSION 1 (bases 1 to 1191)
KEYWORDS EST.
SOURCE Phaeosphaeria nodorum
ORGANISM Phaeosphaeria nodorum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Phaeosphaeriaceae; Phaeosphaeria.
REFERENCE 1 (bases 1 to 1191)
AUTHORS Bindaschledler, L.V., Cooper, R.M., Thomas, S.W., Madrid, M.P. and
Oliver, R.P.
TITLE cDNA library of Phaeosphaeria nodorum grown on wheat cell walls
JOURNAL Unpublished (2005)
COMMENT Contact: Richard Oliver
Australian Centre for Necrotrophic Fungal Pathogens (ACNFP)
Murdoch University
South Street, Murdoch, W.A 6150, Australia
```

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Tel: +0893607404
Email: roliver@murdoch.edu.au.
Location/Qualifiers
1. .1191
/organism="Phaeosphaeria nodorum"
/mol_type="mRNA"
/db_xref="taxon:13684"
/clone_lib="cDNA library of Phaeosphaeria nodorum grown on
wheat Cell walls"

ORIGIN
Query Match 16.5%; Score 893.2; DB 8; Length 1191;
Best Local Similarity 99.2%; Pred. No. 6.e-244;
Matches 919; Conservative 0; Mismatches 3; Indels 4; Gaps 2;

Qy 3207 CAGCTTTTGTTCCTTTAGTGAGGGTTAATTCGAGCTTGGCGTAATCATGGTCATAGCT 3266
Db 114 CAGCTTTTGTTCCTTTAGTGAGGGTTAATTCGAGCTTGGCGTAATCATGGTCATAGCT 173
Qy 3267 GTTTCCTGTGAAATTTGTTATCCGCTCAAAATTCACACAAATACGAGCCGGAAGCAT 3326
Db 174 GTTTCCTGTGAAATTTGTTATCCGCTCAAAATTCACACAAATACGAGCCGGAAGCAT 233
Qy 3327 AAAAGTGAAGCCTGGGTCCTTAATGAGTGAGCTAACTCACATTAATTCGCTTGGCTC 3386
Db 234 AAAAGTGAAGCCTGGGTCCTTAATGAGTGAGCTAACTCACATTAATTCGCTTGGCTC 293
Qy 3387 ACTGCCGCTTCCAGTCGGGAACCTTCGTCGAGCTGCATTAATGAATCGGCCAAG 3446
Db 294 ACTGCCGCTTCCAGTCGGGAACCTTCGTCGAGCTGCATTAATGAATCGGCCAAG 353
Qy 3447 CGCGGGAGAGGCGGTTTGGTATTGGGGCTCTTCGCGCTTCCTCGCTCACTGACTCGCT 3506
Db 354 CGCGGGAGAGGCGGTTTGGTATTGGGGCTCTTCGCGCTTCCTCGCTCACTGACTCGCT 413
Qy 3507 GCCTCTCGCTGTTTCGCTCGCGAGCGGTATCAGCTCACTCAAAAGCGGTAAATACGGTT 3566
Db 414 GCCTCTCGCTGTTTCGCTCGCGAGCGGTATCAGCTCACTCAAAAGCGGTAAATACGGTT 473
Qy 3567 ATCCACAGAAATCAGGGGATAACCCAGGAAGAATCATGTGAGCAAAAGGCCAGCAAAAGGC 3626
Db 474 ATCCACAGAAATCAGGGGATAACCCAGGAAGAATCATGTGAGCAAAAGGCCAGCAAAAGGC 533
Qy 3627 CAGGAACCGTAAAGGCGCGCTTGTGCGGCTTTTCCATAGGCTCCGCCCTCGCTGACGA 3686
Db 534 CAGGAACCGTAAAGGCGCGCTTGTGCGGCTTTTCCATAGGCTCCGCCCTCGCTGACGA 593
Qy 3687 GCATCAAAAATTCGACGCTCAAGTCAGAGGTGGCGAAACCCCGACAGGACTATAAAGATA 3746
Db 594 GCATCAAAAATTCGACGCTCAAGTCAGAGGTGGCGAAACCCCGACAGGACTATAAAGATA 653
Qy 3747 CAGGGGTTTCCCTTGGGAAGCTCCCTCGTCGCTCTCTGTTCCGACCCCTGCGCTTAC 3806
Db 654 CAGGGGTTTCCCTTGGGAAGCTCCCTCGTCGCTCTCTGTTCCGACCCCTGCGCTTAC 713
Qy 3807 CGGATACCTGTCGCGCTTTCCTCCCTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTG 3866
Db 714 CGGATACCTGTCGCGCTTTCCTCCCTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTG 773
Qy 3867 TAGGTATCTCAGTTTCGCTGAGGTTCGCTCCAAAGCTGGGCTGTGTGACGAAACCCCC 3926
Db 774 TAGGTATCTCAGTTTCGCTGAGGTTCGCTCCAAAGCTGGGCTGTGTGACGAAACCCCC 833
Qy 3927 CGTTTCAGCCCGAGCGCTGCGCTTATTCGGGTAACTATCGCTTGGAGTCCAAACCCGTAAG 3986
Db 834 CGTTTCAGCCCGAGCGCTGCGCTTATTCGGGTAACTATCGCTTGGAGTCCAAACCCGTAAG 893
Qy 3987 ACAGGCTTATCCGCTGCGCAGCAGCACTGGTAAACAGGATTAGCAGAGCGAGGTATGT 4046
Db 894 ACAGGCTTATCCGCTGCGCAGCAGCACTGGTAAACAGGATTAGCAGAGCGAGGTATGT 953
Qy 4047 AGCGGCTGCTACAGAGTTCTTGAAGTGGTGGCTTAACTACGGCTTACACTAGAGAAACAGT 4106
Db 953 AGCGGCTGCTACAGAGTTCTTGAAGTGGTGGCTTAACTACGGCTTACACTAGAGAAACAGT 4106
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FEATURES

source

1. .1191

/organism="Phaeosphaeria nodorum"

/mol_type="mRNA"

/db_xref="taxon:13684"

/clone_lib="cDNA library of Phaeosphaeria nodorum grown on wheat Cell walls"

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Db 954 CG--CGTGTACAGAGTTCCTTGAAGTGGTGGCCCTAACTACGGCTACACTAGA--GACAGT 1009
QY 4107 ATTTGGTATCTGGCTCTGCTGAAGC 4132
Db 1010 ATTTGGTATCTGGCTCTGCTGAAGC 1035

RESULT 8
CL076016 885 bp DNA linear GSS 31-DEC-2003
DEFINITION CH216-138F20.RM1.1 CH216 Xenopus tropicalis genomic clone
CH216-138F20, genomic survey sequence.
ACCESSION CL076016
VERSION CL076016.1 GI:40531929
KEYWORDS GSS.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 885)
AUTHORS Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E. and Wilson, R.
TITLE A physical map of the xenopus tropicalis genome
JOURNAL Unpublished (2003)
COMMENT Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert length: 175000 Std Error: 0.00
Seq primer: RM1 TAGGACTCATATAGGAGA
Class: BAC ends
High quality sequence start: 11
High quality sequence stop: 810.
FEATURES
source Location/Qualifiers
1..885
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-138F20"
/sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/notes="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"

ORIGIN
Query Match 15.8%; Score 859.2; DB 10; Length 885;
Best Local Similarity 99.4%; Pred. No. 3.4e-234;
Matches 872; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 3280 AATTGTTATCCGTCACAAATTCACACACATACGAGCCGGAAGCATAAAGTGTAAAGCC 3339
Db 5 AATTGTTATCCGTCACAAATTCACACACATACGAGCCGGAAGCATAAAGTGTAAAGCC 64
QY 3340 TGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGGCTTGGCTCAGTCCCGCTTTC 3399
Db 65 TGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGGCTTGGCTCAGTCCCGCTTTC 124
QY 3400 CAGTCGGGAAACCTGTGTCGCCAGCTGCATTAAATGAATCGGCCAACCGCGGGGAGAGGC 3459
Db 125 CAGTCGGGAAACCTGTGTCGCCAGCTGCATTAAATGAATCGGCCAACCGCGGGGAGAGGC 184
QY 3460 GGTTCGGTATTTGGGCGCTCTTCGGCTTCCTCGCTCAGTACGCTCGCTCGCTCGCTCGTT 3519
Db 185 GGTTCGGTATTTGGGCGCTCTTCGGCTTCCTCGCTCAGTACGCTCGCTCGCTCGCTCGTT 244
QY 3520 CGGCTCGGGGAGCGGTATCAGCTCACTCAAGCGGTAATCGTTATCCACAGATCA 3579
Db 245 CGGCTCGGGGAGCGGTATCAGCTCACTCAAGCGGTAATCGTTATCCACAGATCA 304
QY 3580 GGGGATAACGAGGAAAGAAACATGTGAGCAAAAGGCGCAGCAAAAGGCGAGAACCGGTAAA 3639
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Db 305 GGGGATAACGAGGAAAGAAACATGTGAGCAAAAGGCGCAGCAAAAGGCGAGGAAACCGGTAAA 364
QY 3640 AAGGCGCGCTTGTCTGGCGTTTTTCCATAGCTCCGCCCGCTCAGCAGCATCAAAAAAT 3699
Db 365 AAGGCGCGCTTGTCTGGCGTTTTTCCATAGCTCCGCCCGCTCAGCAGCATCAAAAAAT 424
QY 3700 CGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACACAGGGGTTTCCC 3759
Db 425 CGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACACAGGGGTTTCCC 484
QY 3760 CTTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCC 3819
Db 485 CTTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCC 544
QY 3820 GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGT 3879
Db 545 GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGT 604
QY 3880 TCGGTAGTGTCTGCTCCAAAGCTGGGCTGTGTGCAGAAACCCCGCTTCAGCCCGAC 3939
Db 605 TCGGTAGTGTCTGCTCCAAAGCTGGGCTGTGTGCAGAAACCCCGCTTCAGCCCGAC 664
QY 3940 CGCTGCGCTTATCCGTTAACTATCTCTTGTAGTCCAAACCCGTAAGACAGACTTATCG 3999
Db 665 CGCTGCGCTTATCCGTTAACTATCTCTTGTAGTCCAAACCCGTAAGACAGACTTATCG 724
QY 4000 CCACTGGCAGCAGCCACTGTAAACAGATTAGCAGAGCAGGATATGTAGCGGTGTCTACA 4059
Db 725 CCACTGGCAGCAGCCACTGTAAACAGATTAGCAGAGCAGGATATGTAGCGGTGTCTACA 784
QY 4060 GAGTCTTTGAAAGTGGTGGCTAACTACGCTACACTAGAGAAACAGTATTTGGTATCTGC 4119
Db 785 GAGTCTTTGAAAGTGGTGGCTAACTACGCTACACTAGAGAAACAGTATTTGGTATCTGC 844
QY 4120 GTCTGCTGAAAGCAGTGTACCTTCGGGAAAGAGTTG 4156
Db 845 GCTCTGCTGAAAG-CAGTTACCTTCGGGAAAGAGTGG 880

RESULT 9
DR046031 1195 bp mRNA linear EST 02-JUN-2005
LOCUS FP-8 F02.SBQ cDNA library of Phaseosphaeria nodorum grown on wheat
DEFINITION cell walls Phaseosphaeria nodorum cDNA, mRNA sequence.
ACCESSION DR046031
VERSION DR046031.1 GI:66909867
KEYWORDS EST.
SOURCE Phaseosphaeria nodorum
ORGANISM Phaseosphaeria nodorum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Phaseosphaeriaceae; Phaseosphaeria.
REFERENCE 1 (bases 1 to 1195)
AUTHORS Bindschedler, L.V., Cooper, R.M., Thomas, S.W., Madrid, M.P. and
Oliver, R.P.
TITLE cDNA library of Phaseosphaeria nodorum grown on wheat cell walls
JOURNAL Unpublished (2005)
COMMENT Contact: Richard Oliver
Australian Centre for Necrotrophic Fungal Pathogens (ACNFP)
Murdoch University
South Street, Murdoch, W.A 6150, Australia
Tel: +0893607404
Email: roliver@murdoch.edu.au.
FEATURES
source Location/Qualifiers
1..1195
/organism="Phaseosphaeria nodorum"
/mol_type="mRNA"
/db_xref="taxon:13684"
/clone_lib="cDNA library of Phaseosphaeria nodorum grown on
wheat cell walls"

ORIGIN
Query Match 15.7%; Score 853; DB 8; Length 1195;
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Best Local Similarity 98.2%; Pred. No. 2.3e-232;		Matches 906; Conservative 0; Mismatches 10; Indels 7; Gaps 4;	
QY	3207	CAGCTTTTGTTCCTTTAGTGAGGTTAAATTTTCAGCTTTCGGCTTAATCATGTCATAGCT	3266
Db	169	CAGCTTTTGTTCCTTTAGTGAGGTTAAATTTTCAGCTTTCGGCTTAATCATGTCATAGCT	228
QY	3267	GTTCCTGTGTGAAATGTTTATCCGCTCACAAATTCACACAAATACATAGCAGCCGGAAGCAT	3326
Db	229	GTTCCTGTGTGAAATGTTTATCCGCTCACAAATTCACACAAATACATAGCAGCCGGAAGCAT	298
QY	3327	AAAGTGTAAGCCTTCGGTGCCTTAATGAGTGAGCTAACTCAATTAATTCGGTTCGGCTC	3386
Db	289	AAAGTGTAAGCCTTCGGTGCCTTAATGAGTGAGCTAACTCAATTAATTCGGTTCGGCTC	348
QY	3387	ACTGCCCGCTTTCAGTCGCGGAACCTGTCTGCGAGCTGCATTAATGAATCGGCCAAGC	3446
Db	349	ACTGCCCGCTTTCAGTCGCGGAACCTGTCTGCGAGCTGCATTAATGAATCGGCCAAGC	408
QY	3447	CGCGGGGAGAGCGGTTTGGCTATTGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCT	3506
Db	409	CGCGGGGAGAGCGGTTTGGCTATTGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCT	468
QY	3507	CGCTTCGGTTCGCTCGCGGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGTT	3566
Db	469	CGCTTCGGTTCGCTCGCGGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGTT	528
QY	3567	ATCCACAGATCAGGGGATACCGAGGAAGACATGTGAGCAAAAGCCAGCAAAAGGC	3626
Db	529	ATCCACAGATCAGGGGATACCGAGGAAGACATGTGAGCAAAAGCCAGCAAAAGGC	588
QY	3627	CAGGAACCGTAAAGACCGGTTGCTGGGCTTTTCCATAGGCTCCGCCCTCGACGA	3686
Db	589	CAGGAACCGTAAAGACCGGTTGCTGGGCTTTTCCATAGGCTCCGCCCTCGACGA	648
QY	3687	GCATCAAAAATCGACGCTCAAGTCAGAGTGGCGAAACCCGACAGACTATAAAGATA	3746
Db	649	GCATCAAAAATCGACGCTCAAGTCAGAGTGGCGAAACCCGACAGACTATAAAGATA	708
QY	3747	CCAGGCGTTTCCCGCTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCTCGCGCTTAC	3806
Db	709	CCAGGCGTTTCCCGCTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCTCGCGCTTAC	768
QY	3807	CGGATACCTGTCGCTTTCCTCCCTCGGGAAGGTCGGCTTTCTCATAGCTCACGCTG	3866
Db	769	CGGATACCTGTCGCTTTCCTCCCTCGGGAAGGTCGGCTTTCTCATAGCTCACGCTG	828
QY	3867	TAGGTATCTCAGTTTCGGTGTAGTTCGTTTCGCTCCAAAGCTGGGCTGTGTGACGAAACCCC	3926
Db	829	TAGGTATCTCAGTTTCGGTGTAGTTCGTTTCGCTCCAAAGCTGGGCTGTGTGACGAAACCCC	888
QY	3927	CGTTACGCGCAACCGCTGCGCTTATTCGGTGAATCTATGCTTTCAGTTCGAACCGGTAAAG	3986
Db	889	CGTTACGCGCGACCGCTGCGCTTATTCGGTGAATCTATGCTTTCAGTTCGAACCGGTAAAG	948
QY	3987	ACAGACTTATCGCCACTGCGCAGCAGCACTGTGTAACAGGATTACGAGCGAGGTATGT	4046
Db	949	A-ACGACTTATCGCCACTGCGCAGCAGCACTGTGTAACAGGATTACGAGCGAGGTATGT	1007
QY	4047	AGGCGGTGCTACAGAGTTCTTGAAGTGGTGCCTTAACCTACGGCTACACTAGAGAAGACAGT	4106
Db	1008	AG--CGTGCTACAGAGTTCTTGAAGTGGTGCCTTAACCTACGGCTACACTAGAGAAGACAGT	1062
QY	4107	ATTTGGTATTCGCGCTCTGCTGA	4129
Db	1063	A-TTGGTATTCGCGCTCTGCTGA	1084

RESULT 10
CV983341
LOCUS
DEFINITION UMC-bof_0A01-002-g06 Ovarian Follicle bof Bos taurus cDNA 3', mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

CV983341
CV983341.1 GI:56144062
EST.
Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 951)
Prather,R.S., Antoniou,E., Garverick,H.A., Green,J.A., Lucy,M.C.,
Roberts,R.M., Smith,M.F. and Youngquist,R.S.
USDA Grant NRI-2002-03476: Bovine ESTs: Focus on Female
Reproduction
Unpublished (2002)
Contact: DNA Core Facility (Bovine Project)
Animal Science - RS Prather
University of Missouri-Columbia
M616 Medical Sciences Bldg., Columbia, MO 65212, USA
Tel: (573)882-0428
Fax: (573)884-5552
Email: bovine@net.missouri.edu
POLYA=No.

Location/Qualifiers
1..951
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/dev_stage="Ovarian Follicle"
/clone_lib="bof"
/note="Vector: pSport1; Funding: The production of ESTs
submitted in this project was funded by USDA Grant
MRI-2002-03476 entitled 'Bovine ESTs: Focus on Female
Reproduction' to RS Prather (Primary Investigator), E
Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, MF
Smith and RS Youngquist. Genetic Source: Heifers for the
project were purchased from Circle A Ranch, Iberia, MO
(http://www.circlea ranch.com/home.html). These heifers,
while not registered have known Angus pedigrees going back
at least 4 generations. Samples collected: The samples
consisted of the following: germinal vesicle-stage
oocytes; in vitro derived embryos (2-cell, morula,
blastocyst and nuclear transfer blastocyst); in vivo
blastocysts and conceptuses (days 8, 14, 16 and 18);
corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian
follicles (days 0, non-recruited, recruited, early
selected and preovulatory); oviduct (days 0, 3 and 5);
endometrium (days 5, 8, 14, 16, 18 and 35); and
placenta/embryo from day 35 conceptuses. Expanded
descriptions of how the tissues were collected can be
found at the following URL:
http://genome.mnet.missouri.edu/Bovine/Methods.html.
Library construction (Standard Protocol): All procedures
have been described in detail elsewhere (Soares et al.,
1994; Bonaldo et al., 1996; Jiang et al., 2001). Total
cellular RNA from each sample was isolated by using
STAT-60 reagent (Tel-Test, Friendswood, TX) and the
poly(A)+ RNA was obtained by two rounds of purification
with the Oligotex mRNA isolation kit (Qiagen) according to
the manufacturer's instructions. The libraries were
constructed essentially as described by the manufacturer's
instructions provided with the SuperScript Plasmid System
(Invitrogen, cat. no. 18248-013). Briefly, 1mcg of
poly(A)+ RNA was annealed at c37 degrees with 10mcg of
NotI-tag-dT18 oligonucleotide (GCTGCTCGGCGCGC-tag-T18)
and reverse transcribed at c37 degrees with SuperScript II
(Invitrogen) reverse transcriptase (Jiang et al., 2001).
The 'tag' represents a tissue/stage-specific ten-base
sequence identifier
(http://genome.uiowa.edu/pubsoft/software.html) present in
the oligonucleotide used to prime first-strand synthesis.
Second strand synthesis was performed with T4 DNA
polymerase in the presence of DNA ligase and RNase H.
After second strand synthesis, the double-stranded cDNAs

were ligated to SalI adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs were size selected by passage through cDNA size fractionation columns (Invitrogen-Life Technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pCMV-SPORT6 vector (Invitrogen). After ligation of the inserts, the plasmids were electroporated into DH10B bacteria. Library Construction (PCR Protocol): The amount of mRNA that was recovered from oocytes and embryos was quite limiting and was not sufficient for library production with the standard protocol. Therefore, PCR-based protocol was utilized for producing libraries from sources in which the amount of extracted mRNA was small (oocytes and embryos). Poly-A RNA was isolated by using the MicroPoly(A) Pure kit from Ambion (cat. # 1918). The mRNA was reverse transcribed with a NotI-tag-dT18 oligonucleotide and a SMART oligonucleotide (Clontech) modified to contain a SalI site to generate full-length cDNA with a sequence complementary to the SMART oligonucleotide. Sequences within the SMART and dT oligonucleotides were used as primers to amplify the cDNAs by PCR with pfu turbo polymerase (Stratagene). The resulting PCR products were purified, digested with NotI and SalI and size fractionated by using Chroma Spin-1000 columns (Clontech). Purified cDNA from each PCR reaction was quantitated and mixed on an equimolar basis for ligation into the pCMV-SPORT6 vector. Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality (e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.) and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. After production of the libraries, equal numbers of recombinants from each library were pooled to produce a single mixed library (mega-library) for more extensive sequencing. Bioinformatics work was performed by GK Springer's group at Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: bovine@net.missouri.edu. Ronaldo MF, Lennon G, Soares MB.. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Biotechniques 31:38-42. Soares MB, MF Banaldo, P Jelene, L Su, L Lawton, A Estrantiadis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232. TAG TISSUE=Ovarian Follicle TAG_SEQ=Not found"

ORIGIN

Query Match 15.7%; Score 852.8; DB 8; Length 951;
 Best Local Similarity 99.8%; Pred. No. 2.4e-232;
 Matches 854; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3438 CGGCCAACGGCGGGAGAGCGGTTTGGCTATTGGCGCTCTTCGCTTCCTCGCTCAC 3497
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 Db 2 CGGCCAACGGCGGGAGAGCGGTTTGGCTATTGGCGCTCTTCGCTTCCTCGCTCAC 61
 |||||

QY 3498 TGACTCGCTCGCTCGCTCGCTCGCGCGAGCGGTATCAGCTCACTCAAGGCGGT 3557
 |||||

Db 62 TGACTCGCTCGCTCGCTCGCTCGCGCGAGCGGTATCAGCTCACTCAAGGCGGT 121
 |||||

QY 3558 AATACGGTTATCCACAGATACGGGGATAACGCGAGGAAGAACATGTGAGCAAAAGGCCA 3617

Db 122 AATACGGTTATCCACAGATACGGGGATAACGCGAGGAAGAACATGTGAGCAAAAGGCCA 181
 |||||

QY 3618 GCAAAAAGCCAGGAACCGTAAAGAGCCGGTGTGGCGTGTTCATAGGCTCGGCCC 3677
 |||||

Db 182 GCAAAAGCCAGGAACCGTAAAGAGCCGGTGTGGCGTGTTCATAGGCTCGGCCC 241
 |||||

QY 3678 CCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGCGGAAACCCGACGACT 3737
 |||||

Db 242 CCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGCGGAAACCCGACGACT 301
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QY 3738 ATAAAGATACGAGCGGTTTCCCTCGAAGCTCCCTCGTGGCTCTCTGTTCGACCCCT 3797
 |||||

Db 302 ATAAAGATACGAGCGGTTTCCCTCGAAGCTCCCTCGTGGCTCTCTGTTCGACCCCT 361
 |||||

QY 3798 GCGGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCTCATAG 3857
 |||||

Db 362 GCGGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCTCATAG 421
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QY 3858 CTCACGCTGTAGGTATCTCAGTTTCGGTGTAGTGTTCGCTCCAAGCTGGGCTGTGTGCA 3917
 |||||

Db 422 CTCACGCTGTAGGTATCTCAGTTTCGGTGTAGTGTTCGCTCCAAGCTGGGCTGTGTGCA 481
 |||||

QY 3918 CGAACCCCGGTTACGCGCGACCGCTGCGCTTATCGGTAACTATCGTTGAGTCCAA 3977
 |||||

Db 482 CGAACCCCGGTTACGCGCGACCGCTGCGCTTATCGGTAACTATCGTTGAGTCCAA 541
 |||||

QY 3978 CCGGTTAAGACACGACTTATCGCCACTGCGCAGCAGCCACTGGTAACAGGATTAAGCAGC 4037
 |||||

Db 542 CCGGTTAAGACACGACTTATCGCCACTGCGCAGCAGCCACTGGTAACAGGATTAAGCAGC 601
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QY 4038 GAGGTATGTAGGCGGTCTACAGAGTTCTTGAAGTGGTGGCCCTAACTACGGCTACACTAG 4097
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Db 602 GAGGTATGTAGGCGGTCTACAGAGTTCTTGAAGTGGTGGCCCTAACTACGGCTACACTAG 661
 |||||

QY 4098 AGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGTTGG 4157
 |||||

Db 662 AGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGTTGG 721
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QY 4158 TAGCTCTTCATCCGGCAACCAACACCCTGCTAGCGTGGTGTTCGTTTGTTCGCAAGCA 4217
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Db 722 TAGCTCTTCATCCGGCAACCAACACCCTGCTAGCGTGGTGTTCGTTTGTTCGCAAGCA 781
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QY 4218 GCAGATTACGCGCAGAAAAAGATCTCAAGAAAGATCTTTGATCTTTCTACGGGCTC 4277
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Db 782 GCAGATTACGCGCAGAAAAAGATCTCAAGAAAGATCTTTGATCTTTCTACGGGCTC 841
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QY 4278 TGACGCTCAGAGAAC 4293
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Db 842 TGACGCTCAGTGAAC 857
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RESULT 11
 CX012952
 LOCUS
 DEFINITION
 mRNA sequence.
 CX012952.1 GI:56395363
 EST.
 Canis familiaris (dog)
 SOURCE
 Canis familiaris
 ORGANISM
 Canis familiaris (dog)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 Canis.
 1 (bases 1 to 875)
 AUTHOR
 TITLE
 ESTs from Canis familiaris whole heart (dog)
 JOURNAL
 Unpublished (2004)
 COMMENT
 Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA

```

Tel: 516 367 8884
Fax: 516 367 8874
Email: mcmombie@cshl.org.
Location/Qualifiers
1. .875
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_lib="Whole Heart Library (DOGESTS)"
/notes="Organ: Heart; Vector: pBluescript II SK; Site 1:
EcoRI; Site 2: XhoI; Library constructed using pBluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"

FEATURES             source
Query Match          15.7%; Score 852.6; DB 8; Length 875;
Best Local Similarity 99.0%; Pred. No. 2.7e-232;
Matches 858; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 3427 CATTAAATGAATCGGCCCAACGCGCGGAGAGCGGTTTGGTATTGGCGCTCTTCGCT 3486
DB 8 CCTTAATGAATCGGCCCAACGCGCGGAGAGCGGTTTGGTATTGGCGCTCTTCGCT 67

QY 3487 TCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 3546
DB 68 TCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 127

QY 3547 TCAAAGCGGTATACGGTTATCCACAGATCAGGGGATTAACGCGAGAAACATGTGA 3606
DB 128 TCAAAGCGGTATACGGTTATCCACAGATCAGGGGATTAACGCGAGAAACATGTGA 187

QY 3607 GCRAAGCGCAGCAAAAGGCCAGAACCGTAAAGGCCGTTGCTGGGCTTTTCCAT 3666
DB 188 GCAAAGCGCAGCAAAAGGCCAGAACCGTAAAGGCCGTTGCTGGGCTTTTCCAT 247

QY 3667 AGGCTCGCCCCCTGACGAGCATCAGAAAATCGACGCTCAAGTCAGAGGTGCGCAAC 3726
DB 248 AGGCTCGCCCCCTGACGAGCATCAGAAAATCGACGCTCAAGTCAGAGGTGCGCAAC 307

QY 3727 CCGACAGACTATAAAGATACAGGCTTTCCCTCGAAGCTCCCTCGTGGCTCTCTCT 3786
DB 308 CCGACAGACTATAAAGATACAGGCGTTTCCCTCGAAGCTCCCTCGTGGCTCTCTCT 367

QY 3787 GTTCCGACCTCGCGCTTACCGGATACGTGCGCCCTTCTCCCTTCGGAGCGGTGGG 3846
DB 368 GTTCCGACCTCGCGCTTACCGGATACGTGCGCCCTTCTCCCTTCGGAGCGGTGGG 427

QY 3847 CTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTTCGGTGTAGTGTGCTTCGCTCAAGCTG 3906
DB 428 CTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTTCGGTGTAGTGTGCTTCGCTCAAGCTG 487

QY 3907 GGCTGTGTGACGAAACCCCGCTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGT 3966
DB 488 GGCTGTGTGACGAAACCCCGCTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGT 547

QY 3967 CTTGAGTCCAAACCGGTAAAGACAGACTTATCGGCACCTGGCAGCAGCACTGGTAAACAGG 4026
DB 548 CTTGAGTCCAAACCGGTAAAGACAGACTTATCGGCACCTGGCAGCAGCACTGGTAAACAGG 607

QY 4027 ATTAGCAGCGAGGTATGTAGGCGGTCTACAGAGTTCTTGAAGTGTGGCTTAACTAC 4086
DB 608 ATTAGCAGCGAGGTATGTAGGCGGTCTACAGAGTTCTTGAAGTGTGGCTTAACTAC 667

QY 4087 GGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGGTACCTTCGGA 4146
DB 668 GGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGGTACCTTCGGA 727

RESULT 12
CF269652 LOCUS 1073 bp mRNA linear EST 13-AUG-2003
DEFINITION Fcylcol4844 Fragilariopsis cylindrus SMART cDNA library (Clontech)
Frangilariopsis cylindrus cDNA clone Antarctic 5', mRNA sequence.
ACCESSION CF269652
VERSION CF269652.1 GI:33631539
KEYWORDS EST.
SOURCE Fragilariopsis cylindrus
ORGANISM Fragilariopsis cylindrus
Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
Bacillariophycidae; Bacillariales; Bacillariaceae; Fragilariopsis.
REFERENCE 1 (bases 1 to 1073)
AUTHORS Mock,T. and Valentin,K.
TITLE EST analysis of freezing tolerance in the Antarctic diatom
Fragilariopsis cylindrus: Detection of numerous cold adaption
related genes and gene transfer events
JOURNAL Unpublished (2003)
COMMENT Contact: Mock T
Biological Oceanography
Alfred-Wegener-Institute for Polar and Marine Research
Am Handelshafen 12, D-27570 Bremerhaven, Germany
Tel.: +49 471 4831 1893
Fax: +49 471 4831 1425
Email: tmock@awi-bremerhaven.de
sequence with unknown function
PCR Primers
FORWARD: 5'lambdaTriplex2
BACKWARD: 3'lambdaTriplex2
Seq primer: ctcggaagcgcccatgtgtggt.
FEATURES             source
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/clone="Antarctic"
/clone_lib="Fragilariopsis cylindrus SMART cDNA library
(Clontech)"
/notes="Vector: pTriplex2; total polyA was used for
first-strand synthesis with SMART IV oligos and CDS
III/3'PCR primer. Double strand cDNA synthesis was done by
LD PCR using the following program: 95oc for 5 min
denaturation and subsequent 20 cycles at 95oc (2min) and
68oc (6min). After SfiI digestion the cDNA was
fractionated with CHROMA Spin-400 columns. These cDNAs
were ligated overnight into pTriplex2 vectors."

ORIGIN
Query Match          15.4%; Score 835.6; DB 6; Length 1073;
Best Local Similarity 96.6%; Pred. No. 2.2e-227;
Matches 894; Conservative 0; Mismatches 24; Indels 7; Gaps 4;

QY 3376 GCGTTGGCTCACTGCGCGCTTCCAGTCGGGAAACCTGTCGCCAGCTGCAATATGA 3435
DB 1 GCTTCTGTCTACTGCCCGCTTCCAGTCGGGAAACCTGTCGCCAGCTGCAATATGA 60

QY 3436 ATCGGCCAACCGCGGGGAGAGCGGTTTCGTTATGGCGCTTCCGCTTCCTCGCTC 3495
DB 61 ATCGGCCAACCGCGGGGAGAGCGGTTTCGTTATGGCGCTTCCGCTTCCTCGCTC 120
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|||||
556 GTTTTCCATAGGTCGCGCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAG 615
QY 3717 GTGGCGAAACCCGACGAGACTAAAGATACGAGGCGTTTCCTCGTGAAGCTCCCTCGT 3776
Db 616 GTGGCGAAACCCGACGAGACTAAAGATACGAGGCGTTTCCTCGTGAAGCTCCCTCGT 675
QY 3777 GCGCTCTCCGTTCCGACCGCTGCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGG 3836
Db 676 GCGCTCTCCGTTCCGACCGCTGCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGG 735
QY 3837 AAGCGTGGCGCTTCTCATAGCTCACGCTAGTAGTATCTCAGTTTCGCTGAGTTCGTTTCG 3896
Db 736 AAGCGTGGCGCTTCTCATAGCTCACGCTAGTAGTATCTCAGTTTCGCTGAGTTCGTTTCG 795
QY 3897 CTCGAAGCTGGGCTGTGTGACAGAACCCCGCTTACCGCGAGCGCTGCGCCTTATCCGG 3956
Db 796 CTCGAAGCTGGGCTGTGTGACAGAACCCCGCTTACCGCGAGCGCTGCGCCTTATCCGG 855
QY 3957 TAACTATCGTCTTGAGTCCAAACCGGTAAGACACGACTTATCGCACTGGCAGCAGCCAC 4016
Db 856 TAACTATCGTCTTGAGTCCAAACCGGTAAGACACGACTTATCGCCTTGNAGACCCAC 915
QY 4017 TGSTAAACAGGATTAGCAGACGAGGTATGTAGGCGGTGTACAGAGTCTTGAAGTGGTG 4076
Db 916 TGSTAAACAGGATTAGCAGACGAGGTATGTAGGCGGTGTACAGAGTCTTGAAGTGGTG 974
QY 4077 GCCTAATACGGCTACACTAGAGAAACAGTATTTGGTATCTGCGCTCTGCTGAAGCAGT 4136
Db 975 GCCCAACTACGGCTACCTTAAAAAAACACTATTGGAAATCGGCCCTCCGAAACCCCTT 1034
QY 4137 TACCTTCGGAAGAAGCTTGGTAGCTCTTGATCGGCAACCAACACCGCTGTGTAGCGG 4196
Db 1035 ACCTTCGG--AAAAAAATTTGTACTCTGACCCCCCAA--AAAAACCCCTGTGAACGG 1090
QY 4197 TGGTTTTTTTGTGCAAGCAGCAGATTAGCGCAGAAAAAAGGATCTCAAGAGATCC 4256
Db 1091 GGGTTTTTTTTTGGCCCAACCCCAATCCCCCAAAAAAATTTCCCCCAAAATCTTTT 1150
QY 4257 TTTGATC 4263
Db 1151 TTTTTC 1157
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RESULT 14
LOCUS CL021193
DEFINITION CH216-8A16_RM1.1 CH216 Xenopus tropicalis genomic clone CH216-8A16,
genomic survey sequence.
ACCESSION CL021193
VERSION CL021193.1 GI:40463006
SOURCE GSS.
ORGANISM Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 1025)
Kremiczki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E. and Wilson, R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: RM1 TACCACTCACTATAGGAGA
Class: BAC ends
High quality sequence start: 72
High quality sequence stop: 837.
FEATURES
Location/Qualifiers
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source
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/cell_line="CH216"
/notes="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"

ORIGIN
Query Match 15.2%; Score 823.2; DB 10; Length 1025;
Best Local Similarity 95.7%; Pred. No. 7.8e-224;
Matches 900; Conservative 0; Mismatches 33; Indels 7; Gaps 5;

QY 3237 TTGAGCTTTGGCGTAATCATGTCATAG-CTGTTTCTGTGTGAAATTTGTTATC-CGCTC 3294
Db 87 TGCATATCTTGGCGTAATCATGTCATAGTCTGTTCTGTGTGAAATTTGTTATCTCGCTC 146
QY 3295 ACAATTTCCACACAACATACGAGCGGAAGCATAAAGTGTAAAGCTGGGGTGCCTAATGA 3354
Db 147 ACAATTTCCACACAACCTTACTACCGGAAGCATAAATGTAAAGCGGGGTGCCTAATGA 206
QY 3355 GTGAGCTTAATCACTTAATTTGCGTTGCGCTCACTGCC--GCTTTCCAGTCGGGAAACC 3412
Db 207 GTGACCTAATCACTTAATTTGCGTTGCGCTCACTGCCAGACTTTCCAATCGGAAACC 266
QY 3413 TGTGCTGCAGCTGCAATTAATGAATGCGCCAAACGCGGG--GAGAGCGGTTTGCCTAT 3470
Db 267 TGTGCTGCCAGCTGCATTAATGAATCGGCCAAACGCGGGGAGAGACGCGTTTGCCTAT 326
QY 3471 TGGGCGCTCTTCCGCTTCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCGCG 3530
Db 327 TGGGCGCTCTTCCGCTTCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGAGC 386
QY 3531 AGCGGTATCAGCTCACTCAAAAGCGGTAATACGCTTATCCACAGAAATCAGGGGATACGC 3590
Db 387 AGCGGTATCAGCTCACTCAAAAGCGGTAATACAGTTATCCACAAATCATGGGATAACGC 446
QY 3591 AGAAAGAACATGTGAGCAAAAGCGCAGCAAAAGCGCAGGAAACCGTAAAAAGCGCGTT 3650
Db 447 AGAAAGAACATGTGAGCAAAAGCGCAGCAAAAGCGCAGGAAACCGTAAAAAGCGCGTT 506
QY 3651 GCTTGGGTTTTTCCATAGGCTCGCCCTCGAGAGCATCAAAAAATGAGCCTCAAG 3710
Db 507 ACTGGGCTTTTTCATAAGCTCCGCCCCCTGACGAGCATCAAAAAATGACGCTCAAG 566
QY 3711 TCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACAGGCGTTTCCCTCTGGAAGCTC 3770
Db 567 TCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACAGGCGTTTCCCTCTGGAAGCTC 626
QY 3771 CCTGCTGCTCTCTGTTCCGACCTTACCGGATACCTGTGCGGCTTTTCTCC 3830
Db 627 CCTGCTGCTCTCTGTTCCGACCTTACCGGATACCTGTGCGGCTTTTCTCC 686
QY 3831 TTGGGAAGCGTGGCGCTTCTCATAGCTCAAGTGTAGTATCTCATGTTCCGTTAGGT 3890
Db 687 TTGGGAAGCGTGGCGCTTCTCATAGCTCAAGTGTAGTATCTCATGTTCCGTTAGGT 746
QY 3891 CGTTTCGCTCCAAAGCTGGGCTGTGTGACAGAACCCCGTTTCAGCCGACCGCTCGGCTT 3950
Db 747 CGTTTCGCTCCAAAGCTGGGCTGTGTGACAGAACCCCGTTTCAGCCGACCGCTCGGCTT 806
QY 3951 ATCCGCTAATCTATGCTTGTAGTCCAAACCCGGTAAAGACAGACTTATGCGCACTGGCAGC 4010
Db 807 ATCCGCTAATCTATGCTTGTAGTCCAAACCCGGTAAAGACAGACTTATGCGCACTGGCAGC 866
QY 4011 AGCCACTGGTAAACAGGATTAGCAGAGCGAGTATGTAGGCGGTGCTACAGAGTCTTTGAA 4070
Db 867 AGCCACTGGTAAACAGGATTAGCAGAGCGAGTATGTAGGCGGTGCTACATACTTCTTGA 926
QY 4071 GTGGTGGCCTAACTACGGCTACACTAGAGAAACAGTATTTGGTATCTGCGCTCTGCTGAA 4130
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Db 927 GTGTGGCTTAACCTACGGCTAC-CTAGAAAAACACTATTGGTATCTGCGCTCTCGCGTA 985
QY 4131 GCCAGTTTACCTTCGGAAGAGAGTTGCTAGCTCTTGATCC 4170
Db 986 ACCAGTTTACCTTCGGAAGAGAGTTGCTAGCTCTTGATCC 1025

RESULT 15
AU081044 1163 bp mRNA linear EST 30-JUL-2002
LOCUS AU081044
DEFINITION Oncorhynchus mykiss Kidney infected by infectious
hematopoietic necrosis virus Oncorhynchus mykiss cdna clone KBI,
mRNA sequence.
ACCESSION AU081044
VERSION AU081044.1 GI:6431392
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 1163)
Kono,T., Sakai,M. and LaPatra,S.E.
Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
Hematopoietic Necrosis Virus
Mar. Biotechnol. 2 (5), 493-498 (2001)
Contact: Masahiro Sakai
Faculty of Agriculture
Miyazaki University
1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan
Email: m.sakai@cc.miyazaki-u.ac.jp.

FEATURES
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/clone_lib="Oncorhynchus mykiss Kidney infected by
infectious hematopoietic necrosis virus"
/notes="common name:rainbow trout ; infected by infectious
hematopoietic necrosis virus"

ORIGIN
Query Match 15.1%; Score 820.4; DB 1; Length 1163;
Best Local Similarity 99.8%; Pred. No. 5.2e-223;
Matches 832; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 3207 CAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCGTAAATCATGGTCATAGCT 3266
Db 331 CAGCTTTTGTTCCTTTAGTGAGGGTTAAATTCGAGCTTGGCGTAAATCATGGTCATAGCT 390
QY 3267 GTTTCCTGTGTAATTTATCCGCTCACAATTTCCACACATACGAGCCGGAAGCAT 3326
Db 391 GTTTCCTGTGTAATTTATCCGCTCACAATTTCCACACATACGAGCCGGAAGCAT 450
QY 3327 AAAGTGTAAAGCTGGGGTGCCTAATGAGTGAGCTAACTACATTAATTCGGTTGGGCTC 3386
Db 451 AAAGTGTAAAGCTGGGGTGCCTAATGAGTGAGCTAACTACATTAATTCGGTTGGGCTC 510
QY 3387 ACTGCCCGCTTTCAGTTCGGGAACCTGTCGTCGAGCTGCATTAATGAATCGGCCAACG 3446
Db 511 ACTGCCCGCTTTCAGTTCGGGAACCTGTCGTCGAGCTGCATTAATGAATCGGCCAACG 570
QY 3447 CGCGGGGAGAGGGGTTTGGTATTTGGGCGCTCTTCGCTTTCCTCGCTCACTGACTCGCT 3506
Db 571 CGCGGGGAGAGGGGTTTGGTATTTGGGCGCTCTTCGCTTTCCTCGCTCACTGACTCGCT 630
QY 3507 GCGCTCGGTCTGCTGCGGCTGCGGAGCGGGTATCAGCTCACTCAAGGCGGTAATACGGTT 3566
Db 631 GCGCTCGGTCTGCTGCGGCTGCGGAGCGGGTATCAGCTCACTCAAGGCGGTAATACGGTT 690
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Search completed: February 21, 2006, 00:22:34
Job time : 19475 secs

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; TOPOLOGY: linear									
; MOLECULE TYPE: cdna									
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Query Match 91.4%; Score 4958.2; DB 2; Length 5707;									
Best Local Similarity 99.2%; Pred. No. 0;									
Matches 5007; Conservative 0; Mismatches 4; Indels 37; Gaps 1;									
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DB	647	CCATGGAAAAATCAGAGTCTCCACCCAAATATTATTAAGTGTGCTGCTTTGTGATTCT	706	1433	GAGAGCAGCTGGGATGCCATGACACAGGGCACCACCTGACCGTGTCTTCCCATGCC	1492			
QY	473	TGAAGTGAAGATGCACACATGCTCTCTCGATCTCTCTACCTGGCGCTGTGCTGC	532	1667	GAGAGCAGCTGGGATGCCATGACACGGGACACCACTGACCGTGTCTTCCCATGCC	1726			
DB	707	TGAAGTGAAGATGCACACATGCTCTCTCGATCTCTCTACCTGGCGCTGTGCTGC	766	1493	AGTAGGAAAGGTTACGAGCGCGTTCATTCTCAGCTTGTGAAGATTTTGTGGGCTC	1552			
QY	533	TCACCTTACAGCTCTGCAOAGGCTGGAACGAGAGCGCTCTGCGGGCTGAGCTGGTG	592	1727	AGTAGGAAAGGTTACGAGCGCGTTCATTCTCAGCTTGTGAAGATTTTGTGGGCTC	1786			
DB	767	TCACCTTACAGCTCTGCAOAGGCTGGAACGAGAGCGCTCTGCGGGCTGAGCTGGTG	826	1553	AGCTGCCAGAGCATGAGCAGCATGCTGTGAGCTCCGAGCTGTGATGAGCAGAGGC	1612			
QY	593	ATGCTCTTCAAGTTCGTGTGGAGACAGGGCTTTTATTTCAACAGCCACAGGGTATG	652	1787	AGCTGCCAGAGCATGAGCAGCATGCTGTGAGCTCCGAGCTGTGATGAGCAGAGGC	1846			
DB	827	ATGCTCTTCAAGTTCGTGTGGAGACAGGGCTTTTATTTCAACAGCCACAGGGTATG	886	1613	AAGGCTCAGCTGAGGCGAGGTGGGACAGGTTAAATTAAGAGCTTCCACTCCACT	1672			
QY	653	GCTCCAGCAGTCGGAGGGCGCTCAGACAGGTATCGTGGATGAGTGTCTTCCGAGCT	712	1847	AAGGCTCAGCTGAGGCGAGGTGGGACAGGTTAAATTAAGAGCTTCCACTCCACT	1906			
DB	887	GCTCCAGCAGTCGGAGGGCGCTCAGACAGCATCGTGGATGAGTGTCTTCCGAGCT	946	1673	TATGGAAGGCTCTCTGCACTCACCTGTCTGGGCTGGGGCAGCAGGGCCACTTC	1732			
QY	713	GTGATCTAAGAGGCTGGAGATGATTTGGGAACCCCTCAAGCTGCCAAGTCAAGTCTGCT	772	1907	TATGGAAGGCTCTCTGCACTCACCTGTCTGGGCTGGGGCAGCAGGGCCACTTC	1966			
DB	947	GTGATCTAAGAGGCTGGAGATGATTTGGCAACCCCTCAAGCTGCCAAGTCAAGTCTGCT	1006	1733	CTCACCCCACCTGACACAAAGGCTTTGCTGTGACAGCCAGGACCTCTGTGGCCACAGA	1792			
QY	773	CTGTCCGTGCCAGCCACACGACATGCCAGACATGCCAGACCCAGAGGAGTACATTTGAGA	832	1967	CTCACCCCACCTGACACAAAGGCTTTGCTGTGACAGCCAGGACCTCTGTGGCCACAGA	2026			
DB	1007	CTGTCCGTGCCAGCCACACGACATGCCAGACATGCCAGACCCAGAGGAGTACATTTGAGA	1066	1793	CTCTTATAGATTCGTGTGCCCTAGGAGACAGGGGCTTTCCCTGCTGCGCTCTCTGGC	1852			
QY	833	ACGCAAGTAGAGGAGTGACAGAAACAAAGAACTACAGATGTAGGAAGACCTCTCTGAGG	892	2027	CTCTTATAGATTCGTGTGCCCTAGGAGACAGGGGCTTTCCCTGCTGCGCTCTCTGGC	2086			
DB	1067	ACGCAAGTAGAGGAGTGACAGAAACAAAGAACTACAGATGTAGGAAGACCTCTCTGAGG	1126	1853	CCGGCGACACTCAGAGCTGCCCTATCTGCCCTCTCTTAGATGCTCTCTGGCAGGAGG	1912			
QY	893	AGTGAAGAGTGACATGCCAGCAGGATCCCGGGCTGCAGGAATTCGATGGCCCATCC	952	2087	CCGGCGACACTCAGAGCTGCCCTATCTGCCCTCTCTTAGATGCTCTCTGGCAGGAGG	2146			
DB	1127	AGTGAAGAGTGACATGCCAGCAGGATCCCGGGCTGCAGGAATTCGATGGCCCATCC	1186	1913	CTGCACCTTGGCTTTGGGCTGATCCATATTACCACTGCAGTAGGAGACAGCTGCTGGAAG	1972			
QY	953	ATTGTCCACCGTAATCTTTTAAACATCTTACATGATCACTTTGCAACCACTCTCAG	1012	2147	CTGCACCTTGGCTTTGGGCTGATCCATATTACCACTGCAGTAGGAGACAGCTGCTGGAAG	2206			
DB	1187	ATTGTCCACCGTAATCTTTTAAACATCTTACATGATCACTTTGCAACCACTCTCAG	1246	1973	AAAAGATGATTTTCAACTGAACTACTATCCAGGAGGTTATTGCTTTTATTTGATGGTG	2032			
QY	1013	GATGACAACTTTGTAGGTTCCAGGCTCTGAGGACCTCCACAGCCATGCAACTTTCTAT	1072	2207	AAAAGATGATTTTCAACTGAACTTACTATCCAGGAGGTTATTGCTTTTATTTGATGGTG	2266			
DB	1247	GATGACAACTTTGTAGGTTCCAGGCTCTGAGGACCTCCACAGCCATGCAACTTTCTAT	1306	2033	CTAAGAGTGGTCTTTTCTCAGCTGTAATGATTTTGCCTCATCTGTGTGAAATACACTTTCCA	2092			
QY	1073	TTTGTAAACAATTTCTGTTACTGTTGTGCAAAAGCTCCATGTGACACAGTGTATGTAAG	1132	2267	CTAAGAGTGGTCTTTTCTCAGCTGTAATGATTTTGCCTCATCTGTGTGAAATACACTTTCCA	2326			
DB	1307	TTTGTAAACAATTTCTGTTACTGTTGTGCAAAAGCTCCATGTGACACAGTGTATGTAAG	1366	2093	ATAACAGCACAGCCTCCAAAGGAAATTTCTGCAGGAAGACAGTACCTGGTGTGGGAAG	2152			
QY	1133	TGTACATAAATAATTTTACCTCGTTTGTGTTTGTGTTTAAACCAATGCCCTGTGG	1192	2327	ATAACAGCACAGCCTCCAAAGGAAATTTCTGCAGGAAGACAGTACCTGGTGTGGGAAG	2386			
DB	1367	TGTACATAAATAATTTTACCTCGTTTGTGTTTGTGTTTAAACCAATGCCCTGTGG	1426	2153	TCCTGTGAGCCCTATGTGCTTCAAGCTGAATGGCTGGGACCTGGCTGGGAGAGCAGAT	2212			
QY	1193	AAGGAAACATAAACTTTCAAGAGCATTAATCATCAGTCAATCTGTGCACACCCCTAATG	1252	2387	TCCTGTGAGCCCTATGTGCTTCAAGCTGAATGGCTGGGACCTGGCTGGGAGAGCAGAT	2446			
DB	1427	AAGGAAACATAAACTTTCAAGAGCATTAATCATCAGTCAATCTGTGCACACCCCTAATG	1486	2213	CACATCTCTTTTAAAGAACAAACAGAGGTAGTGTGCACCTGTGTATTACTATT	2272			
QY	1253	CAGTGTCTCTCATCATTTTCCCTGGGCTCTTCCATCTCTCGTGAACCTGGGACTGGGT	1312	2447	CACATCTCTTTTAAAGAACAAACAGAGGTAGTGTGCACCTGTGTATTACTATT	2506			
DB	1487	CAGTGTCTCTCATCATTTTCCCTGGGCTCTTCCATCTCTCGTGAACCTGGGACTGGGT	1546	2273	TACGCGTGTGTGTTCAGTGGCACAATACCTCAACCGGGATATGGAGAGCTATTTCCCAAC	2332			
QY	1313	GCTGGGCTGGGAGCAGGGGTGGGGCTCTCCAGGAGAGATGGCATGGGAGAGTATG	1372	2507	TACGCGTGTGTGTTCAGTGGCACAATACCTCAACCGGGATATGGAGAGCTATTTCCCAAC	2566			
DB	1547	GCTGGGCTGGGAGCAGGGGTGGGGCTCTCCAGGAGAGATGGCATGGGAGAGTATG	1606	2333	CTCTGTGCTGGAGCCCTGATCTGGGGTTTTCCTGTAGCTTAAAGGGTGGCACTGCTTAA	2392			
QY	1373	GGATACTGCTGGGGGGGGGACTCACCTCTGCTGGGCTGCAGGAAGCCCAATTTGGTGCA	1432	2567	CCTCGCTGCTGGAGCCCTGATCTGGGGTTTTCCTGTAGCTTAAAGCGGTGCCAAGCTTAA	2626			
				2393	GTGATTTGTAGAATCAGTAAGGCTGGAAAAGACACACAGATCATTAAGTCCAACTGTGAGCC	2452			
				2627	GTGATTTGTAGAATCAGTAAGGCTGGAAAAGACACACAGATCATTAAGTCCAACTGTGAGCC	2686			
				2453	CCATCCCCACCGGCCCACTGTCACTCAGTGCCACATCCACGCAATTTCTTGAACATCTCC	2512			

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Db 2747 AGGACAGTGACTCCACCCGTCACCAAGCTGTGCTTCAGAGCAGCAGGCTGACAGCTCA 2806
QY 2573 GTGCCAGTTGCATCTCTGTGAAAGAGCTTAAACAGTGCAAGTTTAAACACGAGCTGATTTGTT 2632
Db 2807 GTGCCAGTTGCATCTCTGTGAAAGAGCTTAAACAGTGCAAGTTTAAACACGAGCTGATTTGTT 2866
QY 2633 GATGTGTTGCTCAATCAGTACGTTGAGATGTCATTAACCTTTTGGAGAGTAATTTTCAG 2692
Db 2867 GATGTGTTGCTCAATCAGTACGTTGAGATGTCATTAACCTTTTGGAGAGTAATTTTCAG 2926
QY 2693 GATGGAACACATTTTAAACCTTGAACACAGCCTTTGATTTGGGCTTTGGCATTTGCGAGAAT 2752
Db 2927 GATGGAACACATTTTAAACCTTGAACACAGCCTTTGATTTGGGCTTTGGCATTTGCGAGAAT 2986
QY 2753 TTGACGAAAGATTTGTTTGGGAACAGATGAATGGAATTTTCCACCAACAGAAATTTAAC 2812
Db 2987 TTGACGAAAGATTTGTTTGGGAACAGATGAATGGAATTTTCCACCAACAGAAATTTAAC 3046
QY 2813 ACTTACACAGTTTGTAGTCTGTCTGCTTCTGATATTTCTTAAGATCTCATCATCTCC 2872
Db 3047 ACTTACACAGTTTGTAGTCTGTCTGCTTCTGATATTTCTTAAGATCTCATCATCTCC 3106
QY 2873 CTGCTCTTTGACACAGTCTGCTGACAGGAGTGGAGATCATCAGGTCAGCATCTCTCAG 2932
Db 3107 CTGCTCTTTGACACAGTCTGCTGACAGGAGTGGAGATCATCAGGTCAGCATCTCTCAG 3166
QY 2933 CATCTAGGAGTGTGCACTATGTGTGATGTGACACTTTTGAAGAACTGCTTTGATTTCCCA 2992
Db 3167 CATCTAGGAGTGTGCACTATGTGTGATGTGACACTTTTGAAGAACTGCTTTGATTTCCCA 3226
QY 2993 GGGCTTTCCTCTCTTCCATGACAGGCTCACTATCAGCCCTGAAAGTCCAACTTTCTGAA 3052
Db 3227 GGGCTTTCCTCTCTTCCATGACAGGCTCACTATCAGCCCTGAAAGTCCAACTTTCTGAA 3286
QY 3053 CTTTCCAGACCGTCTGCTGCTGTAGGCTTCCATAGAGGCCACAGGAGCTGTAGCCAG 3112
Db 3287 CTTTCCAGACCGTCTGCTGCTGTAGGCTTCCATAGAGGCCACAGGAGCTGTAGCCAG 3346
QY 3113 GCATGACCTTTTCCAGCCGCTGCTCTGAATCCAGCCTGTGTGCTGGAGGAGCTCTGG 3172
Db 3347 GCATGACCTTTTCCAGCCGCTGCTCTGAATCCAGCCTGTGTGCTGGAGGAGCTCTGG 3406
QY 3173 TCTGGGGTCTCAGTGTAGCCAGGGAACAGCT----- 3206
Db 3407 TCTGGGGTCTCAGTGTAGCCAGGGAACAGCTTTATCGATACCGTCTCGACCTCGAGGGG 3466
QY 3207 -----CAGCTTTTGTCCCTTTAGTGAGGGTTAATTTTCGAGCTTTGGGCTAATCA 3255
Db 3467 GGGCCGGTACCCAGCTTTTGTCCCTTTAGTGAGGGTTAATTTTCGAGCTTTGGGCTAATCA 3526
QY 3256 TGGTCTATAGTGTTCCTGTGTGAAATTTGTTATCCGCTCACAATTTCCACAACATACGA 3315
Db 3527 TGGTCTATAGTGTTCCTGTGTGAAATTTGTTATCCGCTCACAATTTCCACAACATACGA 3586
QY 3316 GCCGGAAGCATAAAGTGTAAAGCTTGGGGTCCCTAATGAGTGAGCTTAACTCAATTAAT 3375
Db 3587 GCCGGAAGCATAAAGTGTAAAGCTTGGGGTCCCTAATGAGTGAGCTTAACTCAATTAAT 3646
QY 3376 GCGTTGGGCTCATGCGCGCTTTCCAGTCGGGAACCTGTGCGTCCAGCTGCATTAATGA 3435
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QY 3436 ATCGGCCAAGCGCGGGAGAGCGGTTTGGCTATTTGGGGCTCTTCCGCTTCTCGCTC 3495
Db 3707 ATCGGCCAAGCGCGGGAGAGCGGTTTGGCTATTTGGGGCTCTTCCGCTTCTCGCTC 3766
QY 3496 ACTGACTCGCTCGCTCGCTGTGCTGCTGCGCGAGCGGTATCAGCTCACTCAAAAGGCG 3555
Db 3767 ACTGACTCGCTCGCTCGCTGTGCTGCGCGAGCGGTATCAGCTCACTCAAAAGGCG 3826

QY 3556 GTAATACGGTTATCCACAGATCAGGGGATAAACGACGAGAAAGAACATGTGAGCAAAAGGC 3615
Db 3827 GTAATACGGTTATCCACAGATCAGGGGATAAACGACGAGAAAGAACATGTGAGCAAAAGGC 3886
QY 3616 CAGCAAAAGGCCAGGAAACCGTAAAGAGCGGCTGCTGGCGTTTTCATAGGCTCCGC 3675
Db 3887 CAGCAAAAGGCCAGGAAACCGTAAAGAGCGGCTGCTGGCGTTTTCATAGGCTCCGC 3946
QY 3676 CCCCCTGACGAGCATCACAAAAATCAGCTCAAGTCAGAGGTGGGAAACCCGACAGGA 3735
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Db 4007 CTATAAAGATACAGGCGTTTCCCCTGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACC 4066
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Db 4187 CACGAAACCCCGCTTCCAGCCCGACCGCTTATCCGCTTAATCTCTTGAGTCC 4246
QY 3976 AACCCGGTAAAGACACGACTTATTCGCACTGGGAGAGCCACTGCTTAACAGGATTAGCAGA 4035
Db 4247 AACCCGGTAAAGACACGACTTATTCGCACTGGGAGAGCCACTGCTTAACAGGATTAGCAGA 4306
QY 4036 GCGAGTATGTAGGCGGTCTCAGAGTTCTTGAAGTGTGGCTTAACAGGCTACACT 4095
Db 4307 GCGAGTATGTAGGCGGTCTCAGAGTTCTTGAAGTGTGGCTTAACAGGCTACACT 4366
QY 4096 AGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTTACCTTCGAAAAAGAGTT 4155
Db 4367 AGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTTACCTTCGAAAAAGAGTT 4426
QY 4156 GGTAGCTCTTGATTCGGGCAAAACAAACCGCTGTGAGGCTGGTGTGTTTGTGTTGCAAG 4215
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QY 4216 CAGCAGATTACCGCAGAAAGAGATCTCAGAGAGATCTTGTGATCTTTCTACGGGG 4275
Db 4487 CAGCAGATTACCGCAGAAAGAGATCTCAGAGAGATCTTGTGATCTTTCTACGGGG 4546
QY 4276 TCTGACGCTCAGAAAGAACTCGTCAAGAGCGGATAGAAGCGGATGCGCTGCGAATCGGGA 4335
Db 4547 TCTGACGCTCAGAAAGAACTCGTCAAGAGCGGATAGAAGCGGATGCGCTGCGAATCGGGA 4606
QY 4336 GCGGCGATACCGTAAAGCAGAGGAGCGGTGAGCCCAATTCGCGCCCAAGCTCTTCAGCA 4395
Db 4607 GCGGCGATACCGTAAAGCAGAGGAGCGGTGAGCCCAATTCGCGCCCAAGCTCTTCAGCA 4666
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QY 4456 TCGATGAATCCAGAAAGCGGCAATTTCCACCATGATATTTCGGAAGCAGGAGCATCGCCA 4515
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QY 4516 TGGGTCAAGCAGAGATCTCTCGCGTGGGATGCGGCTTGAAGCTTGGCGAAACAGTTG 4575
Db 4787 TGGGTCAAGCAGAGATCTCTCGCGTGGGATGCGGCTTGAAGCTTGGCGAAACAGTTG 4846
QY 4576 GCTGGCGAGCGGCTGATGCTTCTGTCAGATCATCTCTGATCGAAGACCGGCTTCC 4635
Db 4847 GCTGGCGAGCGGCTGATGCTTCTGTCAGATCATCTCTGATCGAAGACCGGCTTCC 4906

4036	AGTGAAGATGACATGCCACCGCAGAGATCCCCCGGGCTGCAGGAATTCGATGGCCCATCC	4095
Qy	ATTGTCACCGTAAATGCTTCTAAACATGTTTATCATGATCACTATTGGCCAACCACTCAG	1012
	ATTCGTCACCGTAAATGCTTCTAAACATGTTTACATGATCACATTGGCCAACCACTCAG	4155
Qy	GATGACAACTCTGTAGGTTTCAGGCTGCTGAGGACCTCCACGAGCCCATGCAACTTTCTAT	1072
Db	GATGACAACTCTGTAGGTTTCAGGCTGCTGAGGACCTGCACGAGCCATGCAACTTTCTAT	4215
Qy	TTTGTAACAATTTCTGTTACTGTGTCGCAAGCTCCATGTGCACAGTGATGTAAAG	1132
Db	TTTGTAACAATTTCTGTTACTGTGTCGCAAGCTCCATGTGCACAGTGATGTAAAG	4275
Qy	TGTACATAAATTAATTTATTTACTCTCGTTTGTGTTTGTATTTTAAACCAATGCCCTGTGG	1192
Db	TGTACATAAATTAATTTATTTACTCTCGTTTGTGTTTGTATTTTAAACCAATGCCCTGTGG	4335
Qy	AAGGAACAATAAACTTCAAGAGCAATTAAATCATCATGTCATCTGTCACACCCCTAAATG	1252
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Qy	CAGTTGTTTCTGTTCATCATTTCCCTGGGCTCTCCATCTCTCGCTGACCTGGGACCTGGGT	1312
Db	CAGTTGTTTCTGTTCATCATTTCCCTGGGCTCTCCATCTCTCGCTGACCTGGGACCTGGGT	4455
Qy	GCTGGGCTGGGAGCAGGGGTTGGGGCTCTCCAGGGAGAGATGGCATGGGGAGAGTATG	1372
Db	GCTGGGCTGGGAGCAGGGGTTGGGGCTCTCCAGGGAGAGATGGCATGGGGAGAGTATG	4515
Qy	GGATACTGCTGGGGGGGGGAATCAACCTGCTGTGGGCTGCAGGAAGCCCATGTTGTGCA	1432
Db	GGATACTGCTGGGGGGGGGAATCAACCTGCTGTGGGCTGCAGGAAGCCCATGTTGTGCA	4575
Qy	GAGAGCAGCTGGGATGCCATGACAGGGGCACCCACCTGACCGTGTCTCCCATGCCCC	1492
Db	GAGAGCAGCTGGGATGCCATGACAGGGGCACCCACCTGACCGTGTCTCCCATGCCCC	4635
Qy	AGTAGGAAAAGGGTTACGAGCGCGTTTCATCTCAGCTGTGGAAGATTTGTGGGCTC	1552
Db	AGTAGGAAAAGGGTTACGAGCGCGTTTCATCTCAGCTGTGGAAGATTTGTGGGCTC	4695
Qy	AGCTGCCAGACGATGACGAGCATGCTGTGCAGCTCCGAGCTGTGATGGACAGAGGC	1612
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Qy	AAGGCTCAGCTGAGGCGAGGTGGTGGGCAACAGGTTAAATTAAGAGCTTTCCACTCACT	1672
Db	AAGGCTCAGCTGAGGCGAGGTGGTGGGCAACAGGTTAAATTAAGAGCTTTCCACTCACT	4815
Qy	TATGGAAGCCCTCTCGACCTCAACCTGTCCCTGGGCTGGGGGACGACGAGGCCACTTTC	1732
Db	TATGGAAGCCCTCTCGACCTCAACCTGTCCCTGGGCTGGGGGACGACGAGGCCACTTTC	4875
Qy	CTCACCCCACTGCACAACAAGGCTTTGGCTGCACAGCCAGGACCTCTGTGGCCACAGA	1792
Db	CTCACCCCACTGCACAACAAGGCTTTGGCTGCACAGCCAGGACCTCTGTGGCCACAGA	4935
Qy	CTCTTATAGATTTGCTGTGCCCTTAGGAGACAGGGGGCTTTCCCTGCCTGGCTTCTGGC	1852
Db	CTCTTATAGATTTGCTGTGCCCTTAGGAGACAGGGGGCTTTCCCTGCCTGGCTTCTGGC	4995
Qy	CCGGGCACTGCAGAGCTGCCCTATCTGCTCTCTTATAGATGTCTCTGGCAGGAAG	1912
Db	CCGGGCACTGCAGAGCTGCCCTATCTGCTCTCTTATAGATGTCTCTGGCAGGAAG	5055
Qy	CTGCATTTGGCTGGGGCTGATCCATATTACCACTGCAGTAGGGACAGCACTGCTGGGAAG	1972
Db	CTGCATTTGGCTGGGGCTGATCCATATTACCACTGCAGTAGGGACAGCACTGCTGGGAAG	5115
Qy	AAAAGATGATTTTCACTGAACCTTATCTACCGGCAAGGTTATTTGCTTTATTTGATGGTG	2032
Db	AAAAGATGATTTTCACTGAACCTTATCTACCGGCAAGGTTATTTGCTTTATTTGATGGTG	5175

2033	CTAAGAGTGGTTCTTTTCTCACTGTAAATGATTTTGGCCCTCATGTGTGAATACACTTTTCCA	2099	CTAAGAGTGGTTCTTTTCTCACTGTAAATGATTTTGGCCCTCATGTGTGAATACACTTTTCCA
5176	CTAAGAGTGGTTCTTTTCTCACTGTAAATGATTTTGGCCCTCATGTGTGAATACACTTTTCCA	5235	CTAAGAGTGGTTCTTTTCTCACTGTAAATGATTTTGGCCCTCATGTGTGAATACACTTTTCCA
2093	ATAACAGCAGCAGCCTCCAAAGGGGAATTTCTGCAGGAAGAGACAGATACCTGGTGTGGGAAG	2152	ATAACAGCAGCAGCCTCCAAAGGGGAATTTCTGCAGGAAGAGAGACAGATACCTGGTGTGGGAAG
5236	ATAACAGCAGCAGCCTCCAAAGGGGAATTTCTGCAGGAAGAGAGACAGTACCTGGTGTGGGAAG	5295	ATAACAGCAGCAGCCTCCAAAGGGGAATTTCTGCAGGAAGAGAGACAGTACCTGGTGTGGGAAG
2153	TTCCCTGTGCAGCCCTATGTGCTTCAAGCTGGAATGGCTGGGACTGGCTGGGAGACAGGAT	2212	TTCCCTGTGCAGCCCTATGTGCTTCAAGCTGGAATGGCTGGGACTGGCTGGGAGACAGGAT
5296	TTCCCTGTGCAGCCCTATGTGCTTCAAGCTGGAATGGCTGGGACTGGCTGGGAGACAGGAT	5355	TTCCCTGTGCAGCCCTATGTGCTTCAAGCTGGAATGGCTGGGACTGGCTGGGAGACAGGAT
2213	CACATCTTTCTTAAAAAAGACAAAACAAGAAGGTAGTGTGTGACCTTGCTGTATTTACTATTT	2272	CACATCTTTCTTAAAAAAGACAAAACAAGAAGGTAGTGTGTGACCTTGCTGTATTTACTATTT
5356	CACATCTTTCTTAAAAAAGACAAAACAAGAAGGTAGTGTGTGACCTTGCTGTATTTACTATTT	5415	CACATCTTTCTTAAAAAAGACAAAACAAGAAGGTAGTGTGTGACCTTGCTGTATTTACTATTT
2273	TACGCGTTGTGTTTCAGTGGGCACATACCTCAACGGGGATATGGAGAGCTATTTTCCCCAAC	2332	TACGCGTTGTGTTTCAGTGGGCACATACCTCAACGGGGATATGGAGAGCTATTTTCCCCAAC
5416	TACGCGTTGTGTTTCAGTGGGCACATACCTCAACGGGGATATGGAGAGCTATTTTCCCCAAC	5475	TACGCGTTGTGTTTCAGTGGGCACATACCTCAACGGGGATATGGAGAGCTATTTTCCCCAAC
2333	CCTCGCTGTGGACCTGATCTGGGGTTTTCTGTAGCTTAAAGCGGTGCAACTGCTTAA	2392	CCTCGCTGTGGACCTGATCTGGGGTTTTCTGTAGCTTAAAGCGGTGCAACTGCTTAA
5476	CCTCGCTGTGGACCTGATCTGGGGTTTTCTGTAGCTTAAAGCGGTGCAACTGCTTAA	5535	CCTCGCTGTGGACCTGATCTGGGGTTTTCTGTAGCTTAAAGCGGTGCAACTGCTTAA
2393	GTGATTTGTAAGATCAGTAAGGCTGGAAAAAGACCAAGATCATTTAAGTCCAACGTGCAGCC	2452	GTGATTTGTAAGATCAGTAAGGCTGGAAAAAGACCAAGATCATTTAAGTCCAACGTGCAGCC
5536	GTGATTTGTAAGATCAGTAAGGCTGGAAAAAGACCAAGATCATTTAAGTCCAACGTGCAGCC	5595	GTGATTTGTAAGATCAGTAAGGCTGGAAAAAGACCAAGATCATTTAAGTCCAACGTGCAGCC
2453	CGATCCCAACGGGCCCACTGTCACTCAGTGCACATCCACGCAATTTCTTGAACATCTCC	2512	CGATCCCAACGGGCCCACTGTCACTCAGTGCACATCCACGCAATTTCTTGAACATCTCC
5596	CGATCCCAACGGGCCCACTGTCACTCAGTGCACATCCACGCAATTTCTTGAACATCTCC	5655	CGATCCCAACGGGCCCACTGTCACTCAGTGCACATCCACGCAATTTCTTGAACATCTCC
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5716	GTGCCAGTTGCATCTCTGTGAAAGAGCTTAAACAGTGCAGTTTAAACACGCACTGATTTGT	5775	GTGCCAGTTGCATCTCTGTGAAAGAGCTTAAACAGTGCAGTTTAAACACGCACTGATTTGT
2633	GATGTGGTGTGAAATCAGTACGTTGAGATGTCACTAACTTTTGGAGATTAATTTTCAG	2692	GATGTGGTGTGAAATCAGTACGTTGAGATGTCACTAACTTTTGGAGATTAATTTTCAG
5776	GATGTGGTGTGAAATCAGTACGTTGAGATGTCACTAACTTTTGGAGATTAATTTTCAG	5835	GATGTGGTGTGAAATCAGTACGTTGAGATGTCACTAACTTTTGGAGATTAATTTTCAG
2693	GATGGAACATCTTTAAACCCCTGAACAGCCCTTGTATTTGGCTTGGCATTTGCAGAT	2752	GATGGAACATCTTTAAACCCCTGAACAGCCCTTGTATTTGGCTTGGCATTTGCAGAT
5836	GATGGAACATCTTTAAACCCCTGAACAGCCCTTGTATTTGGCTTGGCATTTGCAGAT	5895	GATGGAACATCTTTAAACCCCTGAACAGCCCTTGTATTTGGCTTGGCATTTGCAGAT
2753	TTGCAGAAAAGATTTGTTGGGAAACAGATGGAATTTCCACAAAACAGAAAAATTAAC	2812	TTGCAGAAAAGATTTGTTGGGAAACAGATGGAATTTCCACAAAACAGAAAAATTAAC
5896	TTGCAGAAAAGATTTGTTGGGAAACAGATGGAATTTCCACAAAACAGAAAAATTAAC	5955	TTGCAGAAAAGATTTGTTGGGAAACAGATGGAATTTCCACAAAACAGAAAAATTAAC
2813	ACTTACACAGTTTGAGTCTGTCTTCGTTTCGATATTTCTTAAAGAAATCTCATCCTCC	2872	ACTTACACAGTTTGAGTCTGTCTTCGTTTCGATATTTCTTAAAGAAATCTCATCCTCC
5956	ACTTACACAGTTTGAGTCTGTCTTCGTTTCGATATTTCTTAAAGAAATCTCATCCTCC	6015	ACTTACACAGTTTGAGTCTGTCTTCGTTTCGATATTTCTTAAAGAAATCTCATCCTCC
2873	CTGCTCTTGGACAGTCTGTCTGACAGGAGGTGGAGGATCATCAGGTCAGCATCCTCAG	2932	CTGCTCTTGGACAGTCTGTCTGACAGGAGGTGGAGGATCATCAGGTCAGCATCCTCAG
6016	CTGCTCTTGGACAGTCTGTCTGACAGGAGGTGGAGGATCATCAGGTCAGCATCCTCAG	6075	CTGCTCTTGGACAGTCTGTCTGACAGGAGGTGGAGGATCATCAGGTCAGCATCCTCAG
2933	CATCTAGGATGTGCACTATGTGTATGGTGTACATTTTAGAGAACTGCTTGCATTTCCCA	2992	CATCTAGGATGTGCACTATGTGTATGGTGTACATTTTAGAGAACTGCTTGCATTTCCCA
6076	CATCTAGGATGTGCACTATGTGTATGGTGTACATTTTAGAGAACTGCTTGCATTTCCCA	6135	CATCTAGGATGTGCACTATGTGTATGGTGTACATTTTAGAGAACTGCTTGCATTTCCCA
2993	GGGCTTTCCCTCTCTTCCATCAGGGCTCACTATCAGCCCTGAAAGTCCAACTTTCTGAA	3052	GGGCTTTCCCTCTCTTCCATCAGGGCTCACTATCAGCCCTGAAAGTCCAACTTTCTGAA
6136	GGGCTTTCCCTCTCTTCCATCAGGGCTCACTATCAGCCCTGAAAGTCCAACTTTCTGAA	6195	GGGCTTTCCCTCTCTTCCATCAGGGCTCACTATCAGCCCTGAAAGTCCAACTTTCTGAA
3053	CTTCCAGACCGTCTGCTCCTCGTAGGCTGTTCCATAGAGGCCACAGGGACTGTAGCCAG	3112	CTTCCAGACCGTCTGCTCCTCGTAGGCTGTTCCATAGAGGCCACAGGGACTGTAGCCAG
6196	CTTCCAGACCGTCTGCTCCTCGTAGGCTGTTCCATAGAGGCCACAGGGACTGTAGCCAG	6255	CTTCCAGACCGTCTGCTCCTCGTAGGCTGTTCCATAGAGGCCACAGGGACTGTAGCCAG


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QY 3113 GCATGACCTTTTCCAGCGCTGCTCTGAATCCAGCACTGCTGGCTGGAGGAGCTCTGG 3172
Db 6256 GCATGACCTTTTCCAGCGCTGCTCTGAATCCAGCACTGCTGGCTGGAGGAGCTCTGG 6315
QY 3173 TCCTGGGGTCTGCTGAGTGAAGCCAGGGAACA 3202
Db 6316 TCCTGGGGTCTGCTGAGTGAAGCCAGGGAACA 6345

RESULT 3
US-09-186-002-16
; Sequence 16, Application US/09186002B
; Patent No. 6489542
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Method for Transforming Plants to Express
; TITLE OF INVENTION: delta-Endotoxins
; FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
; CURRENT APPLICATION NUMBER: US/09/186,002B
; CURRENT FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 8349
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: gene
; LOCATION: (3666)..(5573)
; OTHER INFORMATION: completely synthesized
US-09-186-002-16
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Query Match 32.2%; Score 1748.2; DB 3; Length 8349;
Best Local Similarity 88.0%; Pred. No. 0;
Matches 2023; Conservative 0; Mismatches 28; Indels 248; Gaps 1;
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QY 3241 AGCTTGGCGTAATCATGGTCTATAGCTGTTTCCTGTGTGAATTTGTTATCCGCTCACAAATT 3300
Db 5909 AGCTTGGCGTAATCATGGTCTATAGCTGTTTCCTGTGTGAATTTGTTATCCGCTCACAAATT 5968
QY 3301 CCACACAATACAGAGCCGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGC 3360
Db 5969 CCACACAATACAGAGCCGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGC 6028
QY 3361 TAACTCACAATTAATTCGGTTGCGCTCACTGCCGCTTTCCAGTCGGGAAACCTGTGCTGC 3420
Db 6029 TAACTCACAATTAATTCGGTTGCGCTCACTGCCGCTTTCCAGTCGGGAAACCTGTGCTGC 6088
QY 3421 CAGTGTGATTAATGAATTCGGCCAAACGCGCGGGAGAGCGGTTTGGTATTTGGCGCTCT 3480
Db 6089 CAGTGTGATTAATGAATTCGGCCAAACGCGCGGGAGAGCGGTTTGGTATTTGGCGCTCT 6148
QY 3481 TCAGCTTCTCGCTCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
Db 6149 TCAGCTTCTCGCTCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6208
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Db 6209 GCTCAGCTCAAAAGGCGGTAATACGGTTATCAACAAGATCAGGGGATACGCGAGGAAAGAAC 6268
QY 3601 ATGTGAGCAAAAGCCAGCAAAAGCCAGCAAGCCGTAAGAGCCGCTTTGCTGGCGCTTT 3660
Db 6269 ATGTGAGCAAAAGCCAGCAAAAGCCAGCAAGCCGTAAGAGCCGCTTTGCTGGCGCTTT 6328
QY 3661 TTCCATAGGCTCCGCCCTCCCTGACGAGCATCACAAAATACGAGCTCAAGTCAAGTGAGTGG 3720
Db 6329 TTCCATAGGCTCCGCCCTCCCTGACGAGCATCACAAAATACGAGCTCAAGTCAAGTGAGTGG 6388
QY 3721 CGAAACCCGACAGGACTATAAAGATACAGGCGCTTTCCCTCGGAAGCTCCCTCGTGGC 3780
Db 6389 CGAAACCCGACAGGACTATAAAGATACAGGCGCTTTCCCTCGGAAGCTCCCTCGTGGC 6448
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QY 3781 TCTCTGTTTCCGACCTCGCGCTTACCGGATACCTGTCCGCTTTTCTCCCTTCGGGAAGC 3840
Db 6449 TCTCTGTTTCCGACCTCGCGCTTACCGGATACCTGTCCGCTTTTCTCCCTTCGGGAAGC 6508
QY 3841 GTGGCGCTTTTCTCATAGTCAAGCTGTAGGTATCTCAGTTCGGTGTAGTGTGGTTCGCTCC 3900
Db 6509 GTGGCGCTTTTCTCAATGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGTGTGGTTCGCTCC 6568
QY 3901 AAGCTGGGCTGTGTGACGAAACCCCGCTTACGCGGAGCGGCTTATCCGCTTAAC 3960
Db 6569 AAGCTGGGCTGTGTGACGAAACCCCGCTTACGCGGAGCGGCTTATCCGCTTAAC 6628
QY 3961 TATCGTCTTGAAGTCAACCCCGGTAAACACGACTTATCGCACTGGCAGCAGCACTGGT 4020
Db 6629 TATCGTCTTGAAGTCAACCCCGGTAAACACGACTTATCGCACTGGCAGCAGCACTGGT 6688
QY 4021 AACAGGATTTAGCAGAGCGAGGTATGTAGCGGTGTCTACAGAGTCTTGAAGTGGTGCCT 4080
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Db 6749 AACTACGGCTACACTAGAAAGACAGTATTTGGTATCTCGCTGTCTGAGCAGCACTTACC 6808
QY 4141 TTCCGAAAGAGTGTGTGACGAAACCCCGCTTACGCGCAACCAACCGCTGTGTAGCGGTGT 4200
Db 6809 TTCCGAAAGAGTGTGTGACGAAACCCCGCTTACGCGCAACCAACCGCTGTGTAGCGGTGT 6868
QY 4201 TTTTGTGTGTGCAAGCAGAGATTACGCGCAGAAAAAAGGATCTCAAGAAAGTTCCTTTG 4260
Db 6869 TTTTGTGTGTGCAAGCAGAGATTACGCGCAGAAAAAAGGATCTCAAGAAAGTTCCTTTG 6928
QY 4261 ATCTTTTCTACGGGCTCTGA----- 4280
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QY 4281 ----- 4280
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QY 4281 ----- 4280
Db 7109 AACCTTTTCATAGAAGCGCGGTGGAATCGAAATCTCGTGTATGGCAGTTGGCGTCGCT 7168
QY 4281 -----CGCTCAGAAAGAACTCGTCAAGAAAGCGCATAGA 4312
Db 7169 TGGTGGTCAATTTTCGAACCCAGAGTCCCGCTCAGAAAGAACTCGTCAAGAAAGCGCATAGA 7228
QY 4313 AGCGGATCGCTCGAATCGGAGCGCGCATACCGTAAAGCAAGAGGAGCGGTTCAGCCC 4372
Db 7229 AGCGGATCGCTCGAATCGGAGCGCGCATACCGTAAAGCAAGAGGAGCGGTTCAGCCC 7288
QY 4373 ATTCCGCGCCAGCTCTTACGAAATATCAGCGGTAGCAACGCTATGTCTGTAGCGGT 4432
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Db 7349 CCGCCACACCCAGCGCGCCACAGTCCAGTGAATCAGAAAAAGCGGCACTTTTCCACCATGA 7408
QY 4493 TATTCCGCAAGAGCGCATCCCATATGGGTCAACGAGATCCTCGCGCTCGGGCATGCGCG 4552
Db 7409 TATTCCGCAAGAGCGCATCCCATATGGGTCAACGAGATCCTCGCGCTCGGGCATGCGCG 7468
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Db 7469 CTTTGGCTTGGGCAACAGTTTCGGCTGGCGGCGCCCTGATGCTCTTCGTCAGATCAT 7528
QY 4613 CCTGATCGAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATCGATGTTTTCGCTT 4672
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Db 5476 ATTTGNAACCCAGAGTCCGCTCAGBAGAACTCGTCAAGAGGCGATAGAGCGATGC 5417
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QY 4382 CAAGCTCTTCAGCAATATCAGGGTAGCCAAAGCTATGCTCTGATAGCGGTCCGCCACAC 4441
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QY 4442 CCAGCCGGCCACATGATGAATCCAGAAAAGGGCCCATTTTCCACCATGATATTCGGCA 4501
Db 5296 CCAGCCGGCCACATGATGAATCCAGAAAAGGGCCCATTTTCCACCATGATATTCGGCA 5237
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Db 5236 AGCAGGATCCGCAATGGGTCAAGCAGATCTCGCGTGGGATGCGGCGCTTGGAGCC 5177
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QY 4622 CAAGACCGGCTTCATCCGAGTAGCTGCTCGATCGATGCTTTCGCTTGGTGGTCTGA 4681
Db 5116 CAAGACCGGCTTCATCCGAGTAGCTGCTCGATCGATGCTTTCGCTTGGTGGTCTGA 5057
QY 4682 ATGGCAGGTAGCGGATCAAGCGTATGACGCGCCGCAATTCGATCAGCCATGATGATA 4741
Db 5056 ATGGCAGGTAGCGGATCAAGCGTATGACGCGCCGCAATTCGATCAGCCATGATGATA 4997
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Db 4996 CTTTCTCGGAGGACAGGTGATGACAGGAGATCTGCGCGGCACTTTCGCCCAATA 4937
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QY 4862 TCGTGGCAGCAGATAGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4921
Db 4876 TCGTGGCAGCAGATAGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4817
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Db 4756 CAGAGCAGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4697
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QY 5162 TTACTTTGCGGGCTTCCCACTTACAGAGGCGCCCGAGCTGGCAATTCGCGTTTCG 5221
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Db 4516 TTGCTGTCCATAAAACCGCCAGCTAGCTATCGCCATGTAAAGCCACTGCAAGCTACCT 4457
QY 5282 CTTGCGTATT 5291
Db 4456 GCTTTCCTT 4447

US-09-554-572-3/c
; Sequence 3, Application US/09554572
; Patent No. 6573091
; GENERAL INFORMATION:
; APPLICANT: NATURE TECHNOLOGY, INC.
; TITLE OF INVENTION: CHIMERIC VIRAL PACKAGING SIGNAL WITHOUT GAG GENE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 228,000,30201
; CURRENT APPLICATION NUMBER: US/09/554,572
; CURRENT FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 8574
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: vector
; OTHER INFORMATION: construct for pVLMB3
US-09-554-572-3

Query Match 27.1%; Score 1470; DB 3; Length 8574;
Best Local Similarity 91.7%; Pred. No. 6.7e-314;
Matches 1604; Conservative 0; Mismatches 80; Indels 66; Gaps 2;
QY 3608 CAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGCCTGGCGTTTTTCCATA 3667
Db 7975 CAATAATAGGCCACAGGGTTCTCGAGGGCGGCATCTCGGCGTGTGCTGCGTTTTTCCATA 7916
QY 3668 GGCTCCGCCCCCTGACGAGCATCAAAAATCGAGCTCAAGTCAGAGTGGCGAAACC 3727
Db 7915 GGCTCCGCCCCCTGACGAGCATCAAAAATCGAGCTCAAGTCAGAGTGGCGAAACC 7856
QY 3728 CGACAGACTATAAAGATACAGCGGTTTCCCGCTGGAAGCTCCCTGGTGGCTCTCTG 3787
Db 7855 CGACAGACTATAAAGATACAGCGGTTTCCCGCTGGAAGCTCCCTGGTGGCTCTCTG 7796
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QY 4262 T----- 4262
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4263 -CTTTTCTACGGGCTGACGCTCAGAAAGAACTCGTCAAGAGCGCGATAGAGCGGATGC 4321
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 6835 ATGGGAGGTAGCGGATCAAGGATGACAGGAGATCTTCCCGCGCACCTTCGCCCAATA 6776
 4742 CTCTTCTCGGAGGAGCAAGGTGAGATGACAGGAGATCTTCCCGCGCACCTTCGCCCAATA 4801
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 6715 GCAGCCAGTCCCTTCCCGCTTACGATGACAGGAGATCTTCCCGCGCACCTTCGCCCAATA 6656
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 6475 CCGGAGAACCTGGTCAATCCATCTGTTCAATCATGCGAAAGCATCTCTATCTGCTCT 6416
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 6295 TTGCTGTCCATAAACCGCCAGTCTAGCACTGTTGGGAGGGCGATCGGTGGGGGCT 6236
 5282 CTTGCTGCTT 5291
 6235 GCTTCTCTT 6226

RESULT 6

US-09-380-190A-23/c
 ; Sequence 23, Application US/09380190A
 ; Patent No. 6410220
 ; GENERAL INFORMATION:
 ; APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
 ; TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES
 ; THEREOF
 ; NUMBER OF SEQUENCES: 74
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MUEITING, RAASCH & GEBHARDT, P.A.
 ; STREET: 119 NORTH FOURTH STREET, SUITE 203
 ; CITY: MINNEAPOLIS
 ; STATE: MINNESOTA
 ; COUNTRY: USA
 ; ZIP: 55401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/380,190A
 ; FILING DATE: 26-Aug-1999
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US98/03918
 ; FILING DATE: 28-FEB-98
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MUEITING, ANN M.
 ; REGISTRATION NUMBER: 33,977
 ; REFERENCE/DOCKET NUMBER: 228.00010201
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 612-305-1217
 ; TELEFAX: 612-305-1228
 ; INFORMATION FOR SEQ ID NO: 23:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9093 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
 US-09-380-190A-23

Query Match 27.1%; Score 1470; DB 3; Length 9093;
 Best Local Similarity 91.7%; Pred.No. 6.7e-314;
 Matches 1604; Conservative 0; Mismatches 80; Indels 66; Gaps 2;
 QY 3608 CAAAGGCGCAGCAAAAGCGCAGGAACCGTAAAGAGCGCGTTCGTCGCGTTCCTCCATA 3667
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 DB 8314 TTCGAGCCCTGCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCG 8255
 QY 3848 TTTCTCATAGCTCACGCTAGTATCTCAGTTTCGCTAGTTCGCTTCAGTTCG 3907
 DB 8254 TTTCTCAATGCTCACGCTAGTATCTCAGTTTCGCTAGTTCGCTTCAGTTCG 8195
 QY 3908 GCTGTGTGACGAAACCCCGGTTACGCGCGAGCGCTTATCCGCTTATCCGCTAACTATCGTC 3967
 DB 8194 GCTGTGTGACGAAACCCCGGTTACGCGCGAGCGCTTATCCGCTTATCCGCTAACTATCGTC 8135

QY 3968 TTGAGTCCAAACCCGGTAAAGACAGCACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGA 4027
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 QY 4028 TTAGCAGAGCAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTTAACCTACG 4087
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 QY 4262 T----- 4262
 Db 7834 TAGAAGCGCGGTGGAATCGAATCTCGTGATGGCAGGTTGGCGTCGCTTGGTCGGTC 7775
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 Db 7294 CTTTCTCGCAGGAGCAGGTAGATGACAGGAGATCTCGCCCGGCACTTCGCCCAATA 7235
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 Db 7234 GCAGCCAGTCCCTTCCCGCTTTCAGTGAACAGTCTGAGCAGAGTGGCAGGAAGCGCCG 7175
 QY 4862 TCGTGGCAGCAGATAGCGCGCTGCTGCTGCTGATGTTCAATTACAGGCGCACCGGACA 4921
 Db 7174 TCGTGGCAGCAGATAGCGCGCTGCTGCTGCTGATGTTCAATTACAGGCGCACCGGACA 7115
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QY 4982 CAGAGCAGCGGATTTGTCTGTTGTGCCAGTCATAGCCGAATAGCTCTCCACCAGCGG 5041
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 QY 5102 CTTGATCAGATCTTGTATCCCTCGGCCATCAGATCTTGGCGCAAGAAAGCCATCCAGT 5161
 Db 6934 CTTGATCAGATCTTGTATCCCTCGGCCATCAGATCTTGGCGCAAGAAAGCCATCCAGT 6875
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 QY 5222 TTGCTCTCATAAACCGGCCAGCTAGCAACTGTTGGGAAGGCGATCGGTGGGCGCT 5281
 Db 6814 TTGCTCTCATAAACCGGCCAGCTAGCTATGCCATGTAAAGCCCACTGCAAGCTACCT 6755
 QY 5282 CTTGCGCTATT 5291
 Db 6754 GCTTCTCTT 6745
 RESULT 8
 US-09-554-572-1/c
 ; Sequence 1, Application US/09554572
 ; Patent No. 6573091
 ; GENERAL INFORMATION:
 ; APPLICANT: NATURE TECHNOLOGY, INC.
 ; TITLE OF INVENTION: CHIMERIC VIRAL PACKAGING SIGNAL WITHOUT GAG GENE
 ; TITLE OF INVENTION: SEQUENCES
 ; FILE REFERENCE: 228.00030201
 ; CURRENT APPLICATION NUMBER: US/09/554,572
 ; CURRENT FILING DATE: 2000-09-18
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 9145
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: vector
 ; OTHER INFORMATION: construct for pVLMB1
 US-09-554-572-1
 Query Match 27.1%; Score 1470; DB 3; Length 9145;
 Best Local Similarity 91.7%; Pred. No. 6.7e-314;
 Matches 1604; Conservative 0; Mismatches 80; Indels 66; Gaps 2;
 QY 3608 CAAAAGCCAGCAAAAGGCCAGGAACCGTAAAGAGCCGGTGTGCGGCTTTTCCATA 3667
 Db 8546 CAATAATAGCGCCAGGGTTCTCGAGGCGGCGCATCTCGGCGTGTGCGGCTTTTCCATA 8487
 QY 3668 GGCTCGCGCCCGCTGACGAGCATCACAAAAATCGAGCTCAAGTCAGAGTGGCGAAACC 3727
 Db 8486 GGCTCGCGCCCGCTGACGAGCATCACAAAAATCGAGCTCAAGTCAGAGTGGCGAAACC 8427
 QY 3728 CGACGAGCTATAAGATACAGGCGGTTTCCCGCTGGAAGCTCCCTCGTGGCTCTCTG 3787
 Db 8426 CGACGAGCTATAAGATACAGGCGGTTTCCCGCTGGAAGCTCCCTCGTGGCTCTCTG 8367
 QY 3788 TTCCGACCTCGCGCTTACCGGATACCTGTCGSCCTTCTCCCTCGGGAAGGCGTGGCGC 3847
 Db 8366 TTCCGACCTCGCGCTTACCGGATACCTGTCGSCCTTCTCCCTCGGGAAGGCGTGGCGC 8307
 QY 3848 TTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTTCGGTGTAGGTGCTTTCGCTCCAAGCTGG 3907
 Db 8306 TTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTTCGGTGTAGGTGCTTTCGCTCCAAGCTGG 8247
 QY 3908 GCTGTGTGACGAAACCCCGGTTACGCGGACCGCTGCGCTTATTCGGTAACTATCGTC 3967


```
;
; FILING DATE: 28-FEB-98
; ATTORNEY/AGENT INFORMATION:
; NAME: MUEYING, ANN M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 228.00010201
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5754 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-380-190A-18

Query Match          27.1%; Score 1469.6; DB 3; Length 5754;
Best Local Similarity 92.0%; Pred. No. 7.5e-314;
Matches 1600; Conservative 0; Mismatches 74; Indels 66; Gaps 2;

Qy 3618 GCAAAAGCCAGGAACCGTAAAGCGCGTGTCTGCGCGTGTTCATAGGCTCCGCC 3677
Db |||||
Qy 3678 CCCTGACGAGCATCACAATAATGACGCTCAAGTCAGAGTGGGAAACCCGACAGACT 3737
Db |||||
Qy 5517 CCCTGACGAGCATCACAATAATGACGCTCAAGTCAGAGTGGGAAACCCGACAGACT 5458
Db |||||
Qy 3738 ATAAAGATACAGCGGTTTCCCTCGGAAGCTCCTCGTGGCTCTCTCTGTTCCGACCT 3797
Db |||||
Qy 5457 ATAAAGATACAGCGGTTTCCCTCGGAAGCTCCTCGTGGCTCTCTCTGTTCCGACCT 5398
Qy 3798 GCCCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTCCTCATAG 3857
Db |||||
Qy 5397 GCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTCCTCAATG 5338
Qy 3858 CTACGCTGTAGGTATCTCAGTTCGGTGTAGTGTGCTTCGCTCAAGCTGGGCTGTGTGCA 3917
Db |||||
Qy 5337 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGTGTGCTTCGCTCCAAGCTGGGCTGTGTGCA 5278
Qy 3918 CGAACCCCGCTTCAGCGCCGACCGCTCGCTTATCCGTTAATCTATCTGTGAGTCCAA 3977
Db |||||
Qy 5277 CGAACCCCGCTTCAGCGCCGACCGCTCGCTTATCCGTTAATCTATCTGTGAGTCCAA 5218
Qy 3978 CCCGTTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGAGC 4037
Db |||||
Qy 5217 CCCGTTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGAGC 5158
Qy 4038 GAGGTATGTAGCGGTGTACAGAGTTCTTGAAGTGGTGGCTTAACTACGGCTACACTAG 4097
Db |||||
Qy 5157 GAGGTATGTAGCGGTGTACAGAGTTCTTGAAGTGGTGGCTTAACTACGGCTACACTAG 5098
Qy 4098 AAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAGAGTTGG 4157
Db |||||
Qy 5097 AAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAGAGTTGG 5038
Qy 4158 TAGCTCTTTGATCCGGCAAAACAAACACCGCTGGTGTAGCGGTGTTTTTTTGTTCGAAGCA 4217
Db |||||
Qy 5037 TAGCTCTTTGATCCGGCAAAACAAACACCGCTGGTGTAGCGGTGTTTTTTTGTTCGAAGCA 4978
Qy 4218 GCAGATTACG-----CGCAGAAAAAAGGATCTCAAGAGAGATCCTTTGAT----- 4262
Db |||||
Qy 4977 GCAGATTACGAATTCGCTCCGTCGGGAAACGATTCGGAAGCCCAACCTTTTCAAGAGCGG 4918
Qy 4263 -----CTTTTCTAC 4271
Db 4917 CGGTGGAATCGAATCTCGTATGCGAGGTGGGCGTGGCTGTGTCGATCTATTCGAACC 4858
Qy 4272 GGGGTCTGACCTCAGAGAACTCGTCAAGAGCGGATAGAGGCGGATGCGCTCGGAATC 4331
Db |||||
Qy 4857 CCAGAGTCCGCTCAGAGAACTCGTCAAGAGCGGATAGAGGCGGATGCGCTCGGAATC 4798
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RESULT 11

US-09-380-190A-19/c
; Sequence 19, Application US/09380190A
; Patent No. 6410220
; GENERAL INFORMATION:
; APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
; TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES

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Qy 4332 GGGAGCGCGGATACCGTAAAGACACGAGGAAGCGGTGAGCCATTTCGCCGCCAAGCTCTTC 4391
Db |||||
Qy 4797 GGGAGCGCGGATACCGTAAAGACACGAGGAAGCGGTGAGCCATTTCGCCGCCAAGCTCTTC 4738
Db |||||
Qy 4392 AGCAATATCACCGGTAGCCAAACGCTATGCTCTGATAGCGGTCCGCACACCCAGCGCGGCC 4451
Db |||||
Qy 4737 AGCAATATCACCGGTAGCCAAACGCTATGCTCTGATAGCGGTCCGCACACCCAGCGCGGCC 4678
Qy 4452 ACAGTCGATGAATCCAGAAAGCGGCATTTTCCACCATGATATTCGGCAAGCAGGCATC 4511
Db |||||
Qy 4677 ACAGTCGATGAATCCAGAAAGCGGCATTTTCCACCATGATATTCGGCAAGCAGGCATC 4618
Qy 4512 GCCATGGGTCAACGACGAGATCCTTCGCGCTCGGCATCGCGCTTTCAGCCCTGGCGAAACAG 4571
Db |||||
Qy 4617 GCCATGGGTCAACGACGAGATCCTTCGCGCTCGGCATCGCGCTTTCAGCCCTGGCGAAACAG 4558
Qy 4572 TTCGGCTGGCGGAGCCCTTGATGCTCTTCGTCAGATCATCTGATCGACAGACCGGC 4631
Db |||||
Qy 4557 TTCGGCTGGCGGAGCCCTTGATGCTCTTCGTCAGATCATCTGATCGACAGACCGGC 4498
Qy 4632 TTCATCCGAGTACGTCTCGCTCGATGCGATGTTTTCGCTTGGTGGTTCGATGGGCAAGT 4691
Db |||||
Qy 4497 TTCATCCGAGTACGTCTCGCTCGATGCGATGTTTTCGCTTGGTGGTTCGATGGGCAAGT 4438
Qy 4692 AGCCGGATCAAGCGTATGACAGCGCGCATTTGATCAGCCATGATGGATATCTTCTCGGC 4751
Db |||||
Qy 4437 AGCCGGATCAAGCGTATGACAGCGCGCATTTGATCAGCCATGATGGATATCTTCTCGGC 4378
Qy 4752 AGGAGCAAGTGTAGATGACAGGAGATCTTCGCCCGGCACCTTCGCCCAATAGCAGCCAGTC 4811
Db |||||
Qy 4377 AGGAGCAAGTGTAGATGACAGGAGATCTTCGCCCGGCACCTTCGCCCAATAGCAGCCAGTC 4318
Qy 4812 CCTTCCGCTTTCAGTGACAAAGTCGAGCAGCAGCTGGCGAAGGAAACCGCCGCTCGTGGCCAG 4871
Db |||||
Qy 4317 CCTTCCGCTTTCAGTGACAAAGTCGAGCAGCAGCTGGCGAAGGAAACCGCCGCTCGTGGCCAG 4258
Qy 4872 CCAGATAGCCGCGCTCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4931
Db |||||
Qy 4257 CCAGATAGCCGCGCTCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4198
Qy 4932 GACAAAAGAACCCCGCGCGCCCTTCGCTGACGACCGGAAACACCGCGGCATCAGAGCAGCC 4991
Db |||||
Qy 4197 GACAAAAGAACCCCGCGCGCCCTTCGCTGACGACCGGAAACACCGCGGCATCAGAGCAGCC 4138
Qy 4992 GATTGCTGTGTGTGCCAGTTCATAGCGGAATAGCCTTCACCCAGCGCGCGGAGAAC 5051
Db |||||
Qy 4137 GATTGCTGTGTGTGCCAGTTCATAGCGGAATAGCCTTCACCCAGCGCGCGGAGAAC 4078
Qy 5052 TSCGTGCAATCCATCTGTTCAATCATGCGAAACGATCCTCATCTGCTCTTGTGATCAGA 5111
Db |||||
Qy 4077 TSCGTGCAATCCATCTGTTCAATCATGCGAAACGATCCTCATCTGCTCTTGTGATCAGA 4018
Qy 5112 TCTTGATCCCTCGCGCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCA 5171
Db |||||
Qy 4017 TCTTGATCCCTCGCGCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCA 3958
Qy 5172 GGGCTTCCCAACCTTACCAGAGGGCGCCCGAGCTGGCAATTCGGTTTCGGTGTGTGCA 5231
Db |||||
Qy 3957 GGGCTTCCCAACCTTACCAGAGGGCGCCCGAGCTGGCAATTCGGTTTCGGTGTGTGCA 3898
Qy 5232 TAAACCGCGCAGTCTAGCAACTGTTGGGAAGGCGATCGGTGGCGGCTCTTCGCTATT 5291
Db |||||
Qy 3897 TAAACCGCGCAGTCTAGCTATCGCCATGTAAAGCCCACTGCAAGCTACCTTCTCTT 3838
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QY 5112 TCTGTATCCCTCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCA 5171
DB |||||
DB 4017 TCTGTATCCCTCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCA 3958
QY 5172 GGGCTTCCCAACCTTACCAGAGGGCGCCAGCTGGCAATTCGGTTCGTTGCTGTFCCA 5231
DB |||||
DB 3957 GGGCTTCCCAACCTTACCAGAGGGCGCCAGCTGGCAATTCGGTTCGTTGCTGTFCCA 3898
QY 5232 TAAACCGCCAGCTAGCAACTGTTGGGAGGGCGATCGGTGGGGCCCTCTTCGCTATT 5291
DB |||||
DB 3897 TAAACCGCCAGCTAGCTATCGCCATGTAGCCCACTGAAAGCCCACTGCAAGTACCTGCTTCTCTT 3838

RESULT 12
US-09-380-190A-1/c
; Sequence 1, Application US/09380190A
; Patent No. 6410220
; GENERAL INFORMATION:
; APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
; TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES
; ;
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUEITING, RAASCH & GEBHARDT, P.A.
; STREET: 119 NORTH FOURTH STREET, SUITE 203
; CITY: MINNEAPOLIS
; STATE: MINNESOTA
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/380,190A
; FILING DATE: 26-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/03918
; FILING DATE: 28-FEB-98
; ATTORNEY/AGENT INFORMATION:
; NAME: MUEITING, ANN M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 228.00010201
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6225 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-380-190A-1

Query Match 27.1%; Score 1469.6; DB 3; Length 6225;
Best Local Similarity 92.0%; Pred. No. 7.5e-314;
Matches 1600; Conservative 0; Mismatches 74; Indels 66; Gaps 2;

QY 3618 GCAAAAGCCAGGACCGTAAAGAGCGCGGTTCCTGGCGTTTTCATAGGCTCCGCCC 3677
DB |||||
DB 6048 GCAGGTGACTCGAGGCGCGGCATCTCGCGGTTCCTGGCGTTTTCATAGGCTCCGCCC 5989
QY 3678 CCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGGAAACCCGACGAGCT 3737
DB |||||
DB 5988 CCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGGAAACCCGACGAGCT 5929
QY 3738 ATAAAGATACAGGCGTTTCCCTCGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCT 3797
DB |||||
DB 5928 ATAAAGATACAGGCGTTTCCCTCGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCT 5869

QY 3798 GCGCTTACCGGATACCTGTCGCCCTTCTCCCTTCGGGAAGCGTGGCGCTTCTTCATAG 3857
DB |||||
DB 5868 GCGCTTACCGGATACCTGTCGCCCTTCTCCCTTCGGGAAGCGTGGCGCTTCTTCATAG 5809
QY 3858 CTCAAGCTGTAGGTATCTCAGTTTCGGTGTAGTTCGTTTCGCTCAAGCTGGCTGTGTCGA 3917
DB |||||
DB 5808 CTCAAGCTGTAGGTATCTCAGTTTCGGTGTAGTTCGTTTCGCTCAAGCTGGCTGTGTCGA 5749
QY 3918 CGAACCCCGGTTACGCGGACCGCTGCGCTTATCGGTTAACTATCGTTGAGTCCAA 3977
DB |||||
DB 5748 CGAACCCCGGTTACGCGGACCGCTGCGCTTATCGGTTAACTATCGTTGAGTCCAA 5689
QY 3978 CCGGTTAAGACACGACTTATCGCCACTGGCAGCAGCACCTGGTAAACAGAGTATTAGCAGC 4037
DB |||||
DB 5688 CCGGTTAAGACACGACTTATCGCCACTGGCAGCAGCACCTGGTAAACAGAGTATTAGCAGC 5629
QY 4038 GAGGTATGAGCGGTGCTACAGAGTTCTTGAAGTGTGGCTTAACCTACGGCTACACTAG 4097
DB |||||
DB 5628 GAGGTATGAGCGGTGCTACAGAGTTCTTGAAGTGTGGCTTAACCTACGGCTACACTAG 5569
QY 4098 AAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTTACCTTCGGAAGAGTTGG 4157
DB |||||
DB 5568 AAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTTACCTTCGGAAGAGTTGG 5509
QY 4158 TAGCTCTTGATCCGCGCAACACACCGCTGCTGAGCGTGGTGTGTTTCTGTTGCAAGCA 4217
DB |||||
DB 5508 TAGCTCTTGATCCGCGCAACACACCGCTGCTGAGCGTGGTGTGTTTCTGTTGCAAGCA 5449
QY 4218 GCAGATTACG-----CGCAGAAAAAAGGATCTCAAGAGATCTTTGTAT----- 4262
DB |||||
DB 5448 GCAGATTACGAAATTCGCTCCGCGGAAACGATTCGGAAGCCCAACCTTTCATAGAAGCGG 5389
QY 4263 -----CTTTTCTAC 4271
DB |||||
DB 5388 CGGTGGAATCGAAATCTCGTGTGTCAGAGTTGGCGCTCGCTTGGTTCGTCATTCGAACC 5329
QY 4272 GGGCTCTGACGCTCAGAAGAACTCGTCAAGAGCGGATAGAAGCGGATGCGTTCGGAATC 4331
DB |||||
DB 5328 CCAGGTCCGCTCAGAAGAACTCGTCAAGAGCGGATAGAAGCGGATGCGTTCGGAATC 5269
QY 4332 GGGAGCGGCGATACCGTTAAAGACGAGGAGCGGTTCAGCCATTCGCGCCCAAGCTTTC 4391
DB |||||
DB 5268 GGGAGCGGCGATACCGTTAAAGACGAGGAGCGGTTCAGCCATTCGCGCCCAAGCTTTC 5209
QY 4392 AGCAATATCACGGGTAGCCAAACGCTATGCTCTGATAGCGTTCGCGCAACCCAGCGCGCC 4451
DB |||||
DB 5208 AGCAATATCACGGGTAGCCAAACGCTATGCTCTGATAGCGTTCGCGCAACCCAGCGCGCC 5149
QY 4452 ACAGTCGATGAATCCAGAAAGCGGCATTTTCCACCATGATATTTCGGAAGCAGGCGATC 4511
DB |||||
DB 5148 ACAGTCGATGAATCCAGAAAGCGGCATTTTCCACCATGATATTTCGGAAGCAGGCGATC 5089
QY 4512 GCCATGGGTCAACGACGAGATCTTCGCGCTCGGCGATCGCGCTTCGAGCCCTGGCGAAACAG 4571
DB |||||
DB 5088 GCCATGGGTCAACGACGAGATCTTCGCGCTCGGCGATCGCGCTTCGAGCCCTGGCGAAACAG 5029
QY 4572 TTGCGTGGCGGAGCGGCGGCTTCGTCAGATCATCTGTCAGATCATCTGATCGCAAGACCGGC 4631
DB |||||
DB 5028 TTGCGTGGCGGAGCGGCGGCTTCGTCAGATCATCTGTCAGATCATCTGTCAGCAAGACCGGC 4969
QY 4632 TTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGTTGGTGGTTCGAATGGCGAGGT 4691
DB |||||
DB 4968 TTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGTTGGTGGTTCGAATGGCGAGGT 4909
QY 4692 AGCGGATCAAGGTATGACAGCGCGCGCATTTGTCATCAGCCATGATGATGATCTTCTCGGC 4751
DB |||||
DB 4908 AGCGGATCAAGGTATGACAGCGCGCGCATTTGTCATCAGCCATGATGATGATCTTCTCGGC 4849
QY 4752 AGAGCAGGTGATGATGACAGGAGATCTGCGCGCGCATTTGCGCCAAATAGCAGCCAGTC 4811
DB |||||
DB 4848 AGGAGCAAGGTGATGATGACAGGAGATCTGCGCGCGCATTTGCGCCAAATAGCAGCCAGTC 4789

4812 CTTTCCCGCTTACGTAGCAACAGTCGACAGCAGCTGCGCAAGCAACCGCCGCTCGTGCCAG 4871
4788 CTTTCCCGCTTACGTAGCAACAGTCGACAGCAGCTGCGCAAGCAACCGCCGCTCGTGCCAG 4729
4872 CCACGATAGCCGCGCTCGCTCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 4931
4728 CCACGATAGCCGCGCTCGCTCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 4669
4932 GACAAAAGAACCGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 4991
4668 GACAAAAGAACCGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 4609
4992 GATTGCTGTTGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 5051
4608 GATTGCTGTTGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 4549
5052 TCGCTGCAATCCATCTGTTTCAATCATGCGAAGAGATCCTCATCTGCTCTTGTATCAGA 5111
4548 TCGCTGCAATCCATCTGTTTCAATCATGCGAAGAGATCCTCATCTGCTCTTGTATCAGA 4489
5112 TCTTGATCCCGCTGCGCATCAGATCCTTGGCGGCAAGAACCATCCAGTTTACTTTTGA 5171
4488 TCTTGATCCCGCTGCGCATCAGATCCTTGGCGGCAAGAACCATCCAGTTTACTTTGA 4429
5172 GGGCTTCCCAACCTTACAGAGAGCGCGCCAGCTGCGCAATTCGGTTGCTGCTGCTCA 5231
4428 GGGCTTCCCAACCTTACAGAGAGCGCGCCAGCTGCGCAATTCGGTTGCTGCTGCTCA 4369
5232 TAAACCGCGCGCTGAGCACTGTTGGGAGGCGATCGGTGCGGGCTTCTCGCTATT 5291
4368 TAAACCGCGCGCTGAGCACTGTTGGGAGGCGATCGGTGCGGGCTTCTCGCTATT 4309

RESULT 13

US-09-380-190A-17/c
Sequence 17, Application US/09380190A
Patent No. 6410220
GENERAL INFORMATION:
APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MINNESOTA
COUNTRY: USA
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/380,190A
FILING DATE: 26-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/03918
FILING DATE: 28-FEB-98
ATTORNEY/AGENT INFORMATION:
NAME: MUETING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 228.00010201
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 6321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-380-190A-17
Query Match 27.1%; Score 1469.6; DB 3; Length 6321;
Best Local Similarity 92.0%; Pred. No. 7.5e-314;
Matches 1600; Conservative 0; Mismatches 74; Indels 66; Gaps 2;
3618 GCAAAAGGCGCAGAACCGTAAAGAGCGCGTGTGCTGGCGTGTTCATATAGAGTCCGCCC 3677
6144 GCAGGTGTACTCGAGCGCGCATCTCGCGGTGTGCTGGGTTCATATAGAGTCCGCCC 6085
3678 CCTGACGAGCATACAAAATTCGACGCTCAAGTTCAGAGGTGCGCAACCCGACGAGCT 3737
6084 CCTGACGAGCATACAAAATTCGACGCTCAAGTTCAGAGGTGCGCAACCCGACGAGCT 6025
3738 ATAAAGATACGAGCGGTTCCTCCCTCGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCT 3797
6024 ATAAAGATACGAGCGGTTCCTCCCTCGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCT 5965
3798 GCGCTTACCGGATACCTGTCGCGCTTCCTCCCTCGGAAGCGTGGCGTTCCTCATAG 3857
5964 GCGCTTACCGGATACCTGTCGCGCTTCCTCCCTCGGAAGCGTGGCGTTCCTCATG 5905
3858 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTTCGCTCCAAAGCTGGGCTGTGTGCA 3917
5904 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTTCGCTCCAAAGCTGGGCTGTGTGCA 5845
3918 CGAACCCCGCTTACGCGCGCGCTGCGCTTATCCGGTAACTATCGTTCGAGTCCAA 3977
5844 CGAACCCCGCTTACGCGCGCGCTGCGCTTATCCGGTAACTATCGTTCGAGTCCAA 5785
3978 CCGGTAAACACACGACTTATCGCACTGCGCAGCAGCACTGGTAAACAGATTAAGCAGC 4037
5784 CCGGTAAACACACGACTTATCGCACTGCGCAGCAGCACTGGTAAACAGATTAAGCAGC 5725
4038 GAGTATGTAGCGGTGTACAGAGTTCCTGAAGTGGTGGCCTTAACCTCGGCTACACTAG 4097
5724 GAGTATGTAGCGGTGTACAGAGTTCCTGAAGTGGTGGCCTTAACCTCGGCTACACTAG 5665
4098 AAGACAGTATTTGGTATCTGCGCTGCTGAAGCAGCAGTTCCTCGGAAAAGAGTTGG 4157
5664 AAGGACAGTATTTGGTATCTGCGCTGCTGAAGCAGCAGTTCCTCGGAAAAGAGTTGG 5605
4158 TAGCTCTTGCATCGGCAACCAACCACTGCTGAGCGGTGGTGTGTTGTTGTCAGCA 4217
5604 TAGCTCTTGCATCGGCAACCAACCACTGCTGAGCGGTGGTGTGTTGTTGTCAGCA 5545
4218 GCAGATTACG-----CGCAGAAAAGAGTCTCAAGAGAGATCCTTTGAT----- 4262
5544 GCAGATTACGAAATTCGTCGATGCGAGGTGGCGCTGCTGGTTCGATTCATAGAGCGG 5485
4263 -----CTTTCTAC 4271
5484 CGGTGGAATCGAAATTCGTCGATGCGAGGTGGCGCTGCTGGTTCGATTCATAGAGCGG 5425
4272 GGGTCTGACGCTCAGAAGAACTCGTCAAGAGGCGATAGAGGCGATCGCTCGGAATC 4331
5424 CCAGAGTCCCGCTCAGAAGAACTCGTCAAGAGGCGATAGAGGCGATCGCTCGGAATC 5365
4332 GGGAGCGCGATACCGTAAAGCAACGAGGAGCGGTTCGCGCGCAAGCTCTTC 4391
5364 GGGAGCGCGATACCGTAAAGCAACGAGGAGCGGTTCGCGCGCAAGCTCTTC 5305
4392 AGCAATATCAGCGGTAGCAACGCTATGCTGATAGCGGTTCGCGCAACCGCGGCTC 4451
5304 AGCAATATCAGCGGTAGCAACGCTATGCTGATAGCGGTTCGCGCAACCGCGGCTC 5245
4452 ACAGTCGATGAATCCAGAAAGCGGCTATTTCCACCATGATATTCGGAAGAGCAGCATC 4511
5244 ACAGTCGATGAATCCAGAAAGCGGCTATTTCCACCATGATATTCGGAAGAGCAGCATC 5185


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QY 3978 CCGGTAAGACACGACTTATCGCCACTGCGCAGCAGCCACTGGTAAACAGGATTACGAGC 4037
Db |||||
QY 6354 CCGGTAAGACACGACTTATCGCCACTGCGCAGCAGCCACTGGTAAACAGGATTACGAGC 6295
Db |||||
QY 4038 GAGGTATGTAGGCGGTGCTACAGAGTTCCTGAAAGTGTGGCCCTAACTACGGCTACACTAG 4097
Db |||||
QY 6294 GAGGTATGTAGGCGGTGCTACAGAGTTCCTGAAAGTGTGGCCCTAACTACGGCTACACTAG 6235
Db |||||
QY 4098 AAGAACGATATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTCGGAAGAAGTTGG 4157
Db |||||
QY 6234 AAGGACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTCGGAAGAAGTTGG 6175
Db |||||
QY 4158 TAGCTCTTGTATCCGGCAAAACAAACACCGCTGCTAGCGGTGGTTTTTTTGTGTCGAAGCA 4217
Db |||||
QY 6174 TAGCTCTTGTATCCGGCAAAACAAACACCGCTGCTAGCGGTGGTTTTTTTGTGTCGAAGCA 6115
Db |||||
QY 4218 GCAGATTAACG-----CGCAGAAAAAAGAGTCTCAAGAAAGATCCTTTGAT----- 4262
Db |||||
QY 6114 GCAGATTAACGAAATTCGCTCCGGAAAAACGATTCCGAAGCCCAACCTTTCATAGAAAGCGG 6055
Db |||||
QY 4263 -----CTTTCTAC 4271
Db |||||
QY 6054 CGGTGGAATCGAAATCTCGTGTATGCGAGGTGGGCGTCTGCTGGTCAATTTGCAACC 5995
Db |||||
QY 4272 GGGTCTGACGCTCAGAAAGAACTCGTCAAGAAAGCCGATAGAAAGCCGATGCGCTGCGAATC 4331
Db |||||
QY 5994 CAGAGTCCGCTCAGAAAGAACTCGTCAAGAAAGCCGATAGAAAGCCGATGCGCTGCGAATC 5935
Db |||||
QY 4332 GGGAGCGCGGATACCGTAAAGCAGAGAAAGCGGTAGCCCATTTGCGCCCAAGCTCTTC 4391
Db |||||
QY 5934 GGGAGCGCGGATACCGTAAAGCAGAGAAAGCGGTAGCCCATTTGCGCCCAAGCTCTTC 5875
Db |||||
QY 4392 AGCAATATCAGGGTAGCCAAACGCTATGCTCTGATAGCGGTCCGCCACACCCAGCCGGCC 4451
Db |||||
QY 5874 AGCAATATCAGGGTAGCCAAACGCTATGCTCTGATAGCGGTCCGCCACACCCAGCCGGCC 5815
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Job time : 877 secs